

FIG. 1A

GGCTGCCCGG

AGGGGGCCCGTGCGTGATGCGGGGAGCTGGAAGCCTCGAGCAGCGCGCTTCT
-120

CTGGCCCCGGCGCCATATGCTTGAAGAGCCCGTGCCACCCAGTGCCCCACTGCCCA
-1

1 Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg
ATG GAT CCA CCA CTG AAC CTG TCC TGG TAC GAT GAC GAT CTG GAG AGG
1

* 20 * 30
Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp
CAG AAC TGG AGC CGG CCC TTC AAT GGG TCA GAA GGG AAG GCA GAC
90

Arg Pro His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Ile
AGG CCC CAC TAC AAC TAC TAT GCC ATG CTG CTC ACC CTC CTC ATC
40

50 60
Phe Ile Ile Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser
TTT ATC ATC GTC TTT GGC AAT-GTG CTG GTG TGC ATG GCT GTA TCC
180

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Glu | Lys | Ala | Leu | Gln | Thr | Thr | Thr | Asn | Tyr | Leu | Ile | Val | Ser | |
| GCA | GAG | AAG | GCT | TTG | CAG | ACC | ACC | ACC | AAC | TAC | TTG | ATA | GTC | AGC | |
| | | | | | | | | | | | | | | | 70 |
| Leu | Ala | Val | Ala | Asp | Leu | Val | Ala | Thr | Leu | Val | Met | Pro | Trp | | 90 |
| CTT | GCT | GTG | GCT | GAT | CTT | CTG | GCC | ACA | CTG | GTA | ATG | CCG | TGG | | |
| | | | | | | | | | | | | | | | 270 |
| Val | Val | Tyr | Leu | Glu | Val | Gly | Glu | Trp | Lys | Phe | Ser | Arg | Ile | | |
| GTT | GTC | TAC | CTG | GAG | GTG | GGT | GAG | TGG | AAA | TTC | AGC | AGG | ATT | | |
| | | | | | | | | | | | | | | | 100 |
| His | Cys | Asp | Ile | Phe | Val | Thr | Leu | Asp | Val | Met | Met | Cys | Thr | Ala | 120 |
| CAC | TGT | GAC | ATC | TTT | GTC | ACT | CTG | GAT | GTC | ATG | ATG | TGC | ACA | GCA | |
| | | | | | | | | | | | | | | | 360 |
| Ser | Ile | Leu | Asn | Leu | Cys | Ala | Ile | Ser | Ile | Asp | Arg | Tyr | Thr | Ala | |
| AGC | ATC | CTG | AAC | CTG | TGT | GCC | ATC | AGC | ATT | GAC | AGG | TAC | ACA | GCT | |
| | | | | | | | | | | | | | | | 130 |
| Val | Ala | Met | Pro | Met | Leu | Tyr | Asn | Thr | Arg | Tyr | Ser | Ser | Lys | Arg | 150 |
| GTG | GCA | ATG | CCC | ATG | CTG | TAT | AAC | ACA | CGC | TAC | AGC | TCC | AAG | CGC | |
| | | | | | | | | | | | | | | | 450 |

FIG. 1B

| | |
|---|-----|
| Arg Val Thr Val Met Ile Ala Ile Val Trp Val Leu Ser Phe Thr | 160 |
| CGA GTT ACT ACT ATG ATT GCC ATT GTC TGG GTC CTG TCC TTC ACC | |
| Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn AAT ACA GAC CAG AAT | 180 |
| ATC TCC TGC TGC CCA CTG CTC CTC GGA CTC AAC AAC AAT ACA GAC CAG AAT | 540 |
| Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr Ser Ser Ile | 190 |
| GAG TGT ATC ATT GCC AAC AAC CCT GCC TTT GTG GTC TAC TCC TCC ATT | |
| Val Ser Phe Tyr Val Pro Phe Ile Val Thr Thr Leu Val Tyr Ile | 210 |
| GTC TCA TTC TAC GTG CCC TTC TTC ATC GTC ACT CTG CTG GTC TAT ATC | 630 |
| Lys Ile Tyr Ile Val Leu Arg Lys Arg Lys Arg Arg Val Asn Thr | 220 |
| AAA ATC TAC ATC GTC CTC CTC CGG AAG CGC CGG AAG CGG GTC AAC ACC | |
| Lys Arg Ser Ser Arg Ala Phe Arg Arg Ala Asn Leu Lys Thr Pro Leu | 240 |
| AAG CGC AGC AGT CGA GCT TTC-AGA GCC AAC AAC CTG AAG ACA CCA CTC | 720 |

FIG. 1C

| | | |
|---|-----|-----------------|
| Lys Asp Ala Ala Arg Arg Ala Gln Glu Leu | 250 | Met Glu Met Leu |
| AAG GAT GCT GCC CGC CGA GCT CAG GAG CTG GAA ATG GAG ATG CTG | | |
| Ser Ser Thr Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro | 260 | 270 |
| TCA AGC ACC AGC CCC CCA GAG AGG ACC CGG TAT AGC CCC ATC CCT | | 810 |
| Pro Ser His His Gln Leu Thr Leu Pro Asp Pro Ser His His Gly | 280 | |
| CCC AGT CAC CAC CAG CTC ACT CTC CCT GAT CCA TCC CAC CAC GGC | | |
| Leu His Ser Asn Pro Asp Ser Pro Ala Lys Lys Pro Gly Lys Asn Gly | 290 | 300 |
| CTA CAT AGC AAC CCT GAC AGT CCT GCC GCC AAA CCA CCA GAG AAG AAT GGG | | 900 |
| His Ala Lys Ile Val Asn Pro Arg Ile Ala Lys Phe Phe Glu Ile | 310 | |
| CAC GCC AAG ATT GTC AAT CCC AGG ATT GCC GCC AAG TTC TTC TTT GAG ATC | | |
| Gln Thr Met Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr Met | 320 | 330 |
| CAG ACC ATG CCC AAT GGC AAA ACC CGG ACC TCC TCC AAG ACG ATG | | 990 |

FIG. 1D

| | | | | | | | | | | | | |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----------------------|-----|------|
| Ser Arg | Arg | Lys | Leu | Ser | Gln | Gln | Lys | Lys | Ala | Thr | Gln | |
| ACG | CGC | AGA | AAG | CTC | TCC | CAG | CAG | AAG | AAA | GCC | ACT | CAG |
| | | | | | | | | | | | | 340 |
| Met Leu | Ala | Ile | Val | Leu | Gly | Val | Phe | Ile | Cys | Trp | Leu | 360 |
| ATG | CTT | GCC | ATT | GTT | CTC | GTG | TTC | ATC | ATC | TGG | CTG | Pro |
| | | | | | | | | | | | | CCC |
| | | | | | | | | | | | | 1080 |
| Phe Phe | Ile | Thr | His | Ile | Leu | Asn | Ile | Cys | Asp | Cys | Asn | Ile |
| TTC | TTC | ATC | ACG | CAC | ATC | CTG | AAT | ATA | TGT | GAT | TGC | ATC |
| | | | | | | | | | | | | 370 |
| Pro Pro | Val | Leu | Tyr | Ser | Ala | Phe | Thr | Trp | Leu | Gly | Tyr | Val |
| CCA | CCA | GTC | CTC | TAC | AGC | GCC | TTC | ACA | TGG | CTG | TAT | GTC |
| | | | | | | | | | | | | AAC |
| | | | | | | | | | | | | 1170 |
| Ser Ala | Val | Asn | Pro | Ile | Ile | Ile | Tyr | Thr | Phe | Asn | Ile | Glu |
| AGT | GCC | GTC | AAC | CCC | ATC | ATC | TAC | ACC | TTC | AAC | ATC | GAG |
| | | | | | | | | | | | | TTC |
| | | | | | | | | | | | | 400 |
| Arg Lys | Ala | Phe | Met | Lys | Ile | Leu | His | Cys | | | | |
| CGC | AAG | GCC | TTC | ATG | AAG | ATC | TTG | CAC | TGC | TGAGTCTGCCCCCTTGCCCTG | | 1264 |

FIG. 1E

CACAGCAGCTGCTTCCCACCTCCCTGCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG
TGGGCAGAAAGCCCAGATGAACCTTGGCCTTCTCTCGACCCCTGCAGGCCCTGCAGTGTTA
1383
GCTTGGCTCGATGCCCCCTCTCTGCCCACACACCCCTCATCTCTGCCAGGGTAGGGCCAGGG
AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCATGGCTCAGGGCAGCTCACAGAGTGC
1502
CCCTCTCATATCCAGACCCCTGTCTCCTTGGCACCACCAAGATGCAGCGGCCTTCCTTGACC
TTCCTCTTGGCACAGAAACTAGCTCAGTGGTCGAGCACACCCCTGATCGCTGGCTTGGCC
1621
TGGCCCTTGCTTGCCCTGTGCCGGATCAGGTGGTGGGAGGGAGCGCACACGTTCTTACTTT
ATAGGAACCATAGGAAAGCAGGGAACACGCCAAGTCTCCAGGCACATCAGTGTGAGG
1740
AGACACATAAACACCAGGTAGCTCCATGGACCCAGAGAACTGAGGCTGAAAAATC
TGTTTCCACTCCAACCTAGTGTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG
1859

FIG. 1F

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGGAAACAACCTCTA
ATCCTCAAGGGCCCAAGAGAACTCTGTAAAGAGAAAAATAGGCTGATCTCCCTCTACTCT
CCAATCCACTCCACCACCTTCTTGATATACCTTGGATGTATCCATTCCTCACAGCAAATG 1978
CTGGCCAGTCAGGCCTTGGACCAGTGTGGAGTTGAAGCTGGATGTGGTAACTTGGGGCT
CTTTGGGGCTGGGGGGTGTAAACATCGTCTCTCTTCCATATCTCTTCCCTTCCCAGTG 2097
CCTCTGCCCTTAGAAGAGGCTGTGGATGGGGTGGTGGGACTGCTGATACCATTTGGGCCCTGG
CCCTGAATGAGGAGGGAAGCTGCAGTTTGGAGGGTCTGGGATCCAACTCTGTAAACAT 2216
CACTATACCTGTACCAAAACTAATAAAACCTTGACAAGAGTCAAAAAA 2317

FIG. 1G

FIG. 2

I

MD... [P]... [N]... [S]... [W]... [Y]... [D]... [D]... [L]... [E]... [R]... [Q]... [N]... [W]... [S]... [R]... [P]... [F]... [N]... [G]... [S]... [E]... [G]... [K]... [A]... [D]... [R]... [P]... [H]... [Y]... [N]... [Y]... [A]... [M]... [I]... [L]... [I]... [F]... [I]... [F]... [G]... [N]... [V]... [L]... [C]... [M]... [A]... [V]... [S]... [R]... [E]... [K]... [A]... [L]... [Q]... [I]... [T]... [N]...
MGP... [P]... [Q]... [N]... [D]... [S]... [D]... [F]... [L]... [T]... [T]... [N]... [G]... [S]... [H]... [V]... [P]... [D]... [H]... [D]... [V]... [T]... [E]... [E]... [R]... [D]... [E]... [A]... [W]... [V]... [G]... [M]... [A]... [I]... [M]... [S]... [V]... [I]... [V]... [A]... [I]... [F]... [G]... [N]... [V]... [L]... [C]... [M]... [A]... [V]... [S]... [R]... [E]... [K]... [A]... [L]... [Q]... [I]... [T]... [N]...
MGS... [L]... [Q]... [P]... [O]... [A]... [C]... [N]... [A]... [S]... [M]... [N]... [G]... [T]... [E]... [A]... [P]... [G]... [G]... [G]... [A]... [R]... [A]... [T]... [P]... [Y]... [S]... [L]... [Q]... [V]... [T]... [L]... [T]... [V]... [C]... [L]... [A]... [C]... [L]... [L]... [M]... [L]... [T]... [V]... [F]... [G]... [N]... [V]... [L]... [C]... [M]... [A]... [V]... [S]... [R]... [E]... [K]... [A]... [L]... [Q]... [I]... [T]... [N]...
MDV... [L]... [S]... [P]... [Q]... [Q]... [N]... [T]... [T]... [S]... [P]... [P]... [A]... [P]... [E]... [T]... [G]... [G]... [N]... [T]... [G]... [I]... [S]... [D]... [V]... [T]... [V]... [S]... [Y]... [Q]... [V]... [I]... [T]... [S]... [L]... [I]... [G]... [I]... [L]... [I]... [F]... [C]... [A]... [V]... [I]... [G]... [N]... [A]... [Q]... [W]... [A]... [A]... [L]... [E]... [R]... [S]... [L]... [O]... [N]... [V]... [A]... [N]...
MNT... [S]... [A]... [P]... [P]... [A]... [V]... [S]... [N]... [I]... [T]... [V]... [L]... [A]... [P]... [G]... [K]... [G]... [P]... [W]... [Q]... [V]... [A]... [S]... [G]... [L]... [D]... [S]... [N]... [A]... [T]... [G]... [I]... [T]... [A]... [F]... [S]... [M]... [P]... [G]... [W]... [Q]... [L]... [A]... [W]... [T]... [A]... [A]... [Y]... [A]... [L]... [V]... [L]... [V]... [A]... [M]... [G]... [N]... [A]... [I]... [W]... [I]... [L]... [A]... [H]... [Q]... [R]... [M]... [I]... [T]... [N]...
MGACV... [V]... [M]... [T]... [D]... [I]... [N]... [S]... [G]... [L]... [D]... [S]... [N]... [A]... [T]... [G]... [I]... [T]... [A]... [F]... [S]... [M]... [P]... [G]... [W]... [Q]... [L]... [A]... [W]... [T]... [A]... [A]... [Y]... [A]... [L]... [V]... [L]... [V]... [A]... [M]... [G]... [N]... [A]... [I]... [W]... [I]... [L]... [A]... [H]... [Q]... [R]... [M]... [I]... [T]... [N]...
II

II

LIVSLAMADITHVATL [M] [W] [V] [V] [L] [E] [V] [C] [M] [F] [S] [R] [I] [H] [C] [D] [I] [F] [V] [T] [D] [W] [M] [C] [T] [A] [S] [I] [N] [L] [C] [A] [I] [S] [I] [Q] [R] [Y] [A] [V] [A] [M] [I] [T] [M] [T] [R] [Y] [S] [S] [K] [R]
FIVSLACADLV [M] [G] [I] [A] [V] [F] [G] [A] [S] [H] [I] [M] [K] [M] [N] [F] [G] [N] [F] [C] [E] [F] [T] [S] [I] [Q] [M] [C] [V] [F] [A] [S] [I] [E] [T] [L] [C] [U] [A] [V] [Q] [R] [Y] [A] [I] [T] [S] [E] [F] [K] [Y] [Q] [S] [L] [T] [K] [N] [K] [A]
LIVSLASADLV [V] [A] [T] [L] [V] [I] [F] [F] [S] [L] [A] [N] [E] [M] [Q] [W] [M] [E] [G] [K] [T] [C] [E] [I] [Y] [A] [L] [D] [V] [L] [F] [T] [S] [I] [V] [H] [L] [C] [A] [I] [S] [I] [Q] [R] [Y] [A] [I] [T] [S] [E] [F] [K] [Y] [Q] [S] [L] [T] [K] [N] [K] [A]
LIVSLAV [D] [I] [M] [V] [S] [V] [L] [V] [I] [P] [M] [A] [A] [L] [Y] [Q] [M] [N] [N] [W] [L] [G] [Q] [V] [T] [C] [D] [I] [F] [A] [L] [D] [V] [L] [F] [T] [S] [I] [V] [H] [L] [C] [A] [I] [S] [I] [Q] [R] [Y] [A] [I] [T] [S] [E] [F] [K] [Y] [Q] [S] [L] [T] [K] [N] [K] [A]
FLLSLACADLV [I] [G] [H] [F] [S] [M] [N] [Y] [T] [T] [Y] [L] [M] [Q] [I] [M] [A] [L] [G] [T] [A] [C] [D] [I] [W] [L] [A] [D] [V] [A] [S] [N] [A] [S] [V] [M] [N] [L] [I] [I] [S] [E] [Q] [R] [Y] [A] [I] [T] [S] [E] [F] [K] [Y] [Q] [S] [L] [T] [K] [N] [K] [A]
FIVSLALADLV [C] [M] [A] [F] [N] [A] [F] [V] [Y] [A] [S] [H] [I] [M] [E] [G] [R] [A] [F] [C] [Y] [F] [Q] [N] [L] [F] [P] [I] [T] [A] [M] [F] [V] [S] [I] [Y] [S] [M] [T] [A] [I] [A] [Q] [R] [Y] [A] [I] [T] [S] [E] [F] [K] [Y] [Q] [S] [L] [T] [K] [N] [K] [A]
IV

IV

VTV [M] [A] [I] [V] [W] [V] [I] [S] [T] [I] [S] [C] [P] [L] [L] [F] [G] [L] [N] [N] [T] [D]... [Q] [N] [E] [C] [I] [A] [N] [P] [A] [F] [V] [V] [Y] [S] [S] [I] [M] [S] [F] [Y] [V] [P] [I] [V] [T] [L] [L] [V] [V] [I] [K] [I] [V] [L] [R] [K] [R] [K] [R] [V] [N] [T] [R]... (111)
RMV [I] [L] [M] [W] [V] [S] [L] [T] [S] [F] [I] [P] [I] [Q] [M] [H] [W] [Y] [R] [A] [T] [H]... [Q] [K] [A] [I] [D] [C] [Y] [H] [R] [E] [T] [C] [C] [D] [F] [T] [N] [Q] [A] [V] [A] [I] [M] [S] [I] [V] [S] [F] [Y] [V] [P] [I] [V] [T] [L] [L] [V] [V] [I] [K] [I] [V] [L] [R] [K] [R] [K] [R] [V] [N] [T] [R]... (111)
KAI [I] [T] [V] [W] [V] [I] [S] [A] [V] [I] [S] [F] [P] [L] [I] [S] [I] [E] [K] [K] [G] [G]... [G] [G] [P] [Q] [P] [A] [E] [R] [C] [E] [I] [N] [D] [Q] [K] [W] [Y] [I] [S] [S] [C] [I] [G] [S] [F] [A] [P] [O] [I] [M] [L] [V] [V] [I] [K] [I] [V] [L] [R] [K] [R] [K] [R] [V] [N] [T] [R]... (111)
ALT [S] [L] [T] [M] [I] [G] [H] [I] [S] [I] [P] [M] [L] [G] [W] [R] [T] [P] [E] [D] [R]... [S] [D] [P] [D] [A] [C] [T] [I] [S] [K] [D] [M] [G] [Y] [T] [I] [Y] [S] [T] [F] [G] [A] [F] [Y] [I] [P] [I] [L] [M] [L] [V] [I] [K] [I] [V] [L] [R] [K] [R] [K] [R] [V] [N] [T] [R]... (111)
ALM [I] [G] [L] [A] [W] [V] [S] [E] [V] [L] [W] [A] [P] [A] [I] [L] [F] [W] [Q] [Y] [L] [V] [G] [E]... [R] [T] [V] [L] [A] [G] [Q] [C] [Y] [I] [Q] [F] [L] [S] [Q] [P] [I] [T] [F] [G] [T] [A] [M] [A] [F] [Y] [L] [P] [V] [T] [M] [C] [T] [I] [M] [W] [I] [R] [E] [T] [E] [N] [R] [A] [E] [L]... (110)
AV [I] [A] [G] [I] [M] [L] [V] [A] [L] [A] [F] [P] [Q] [C] [F] [Y] [S] [T] [I] [T] [D] [E] [G] [A] [T] [K] [C] [V] [V] [A] [W] [P] [E] [D] [S] [G] [G] [K] [M] [L] [L] [Y] [H] [I] [V] [I] [A] [L] [I] [Y] [E] [L] [P] [V] [W] [V] [M] [F] [V] [A] [M] [S] [V] [I] [G] [L] [T] [W] [R] [S] [V] [P] [G]... (12) -
V

VI

-KEKKATQM [A] [I] [V] [I] [G] [M] [F] [I] [C] [W] [L] [P] [F] [F] [I] [T] [H] [I] [N] [I] [H] [O] [C] [N]... [I] [P] [P] [V] [L] [Y] [S] [A] [F] [T] [L] [G] [Y] [V] [N] [S] [A]... [V] [N] [P] [I] [Y] [T] [I] [E] [N] [I] [E] [F] [R] [N] [A] [F] [K] [I] [D] [H] [C]
-KEKKALK [T] [I] [G] [I] [M] [C] [I] [F] [T] [L] [C] [W] [L] [P] [F] [F] [I] [V] [N] [I] [H] [V] [I] [Q] [D] [N] [L]... [I] [P] [K] [E] [V] [Y] [I] [L] [N] [W] [L] [G] [Y] [V] [N] [S] [A]... [P] [N] [P] [I] [Y] [C] [R] [S] [P] [D] [E] [R] [I] [A] [F] [O] [E] [I] [L] [C] [L]... (36)
-REKKRT [F] [V] [I] [A] [V] [I] [C] [M] [F] [V] [V] [C] [W] [P] [F] [F] [E] [T] [Y] [I] [T] [A] [V] [G] [C] [S]... [V] [P] [R] [T] [E] [K] [F] [F] [P] [M] [E] [G] [Y] [C] [N] [S] [S]... [I] [N] [P] [V] [I] [Y] [T] [I] [F] [N] [H] [D] [F] [R] [R] [A] [F] [K] [I] [L] [C] [R] [C]... (6)
-REKKRT [V] [K] [T] [Q] [I] [M] [C] [I] [F] [T] [L] [C] [W] [L] [P] [F] [F] [I] [V] [A] [L] [V] [P] [P] [C] [E] [S] [S]... [H] [M] [P] [I] [L] [G] [A] [I] [N] [W] [L] [G] [Y] [N] [S] [L]... [I] [N] [P] [V] [I] [Y] [A] [E] [N] [K] [D] [F] [O] [N] [A] [F] [K] [I] [C] [N] [F] [C] [R] [Q]
-KEKKART [S] [A] [I] [L] [L] [A] [F] [I] [V] [T] [M] [I] [N] [M] [V] [L] [V] [S] [T] [F] [C] [K] [D] [C]... [V] [E] [T] [I] [W] [E] [L] [G] [Y] [M] [I] [G] [Y] [N] [S] [T]... [I] [N] [P] [M] [C] [H] [A] [L] [Q] [N] [K] [A] [F] [R] [D] [I] [F] [R] [I] [L] [H] [C] [R]... (24)
-ARKK [F] [V] [K] [T] [M] [V] [I] [V] [V] [T] [F] [A] [I] [C] [W] [L] [P] [Y] [H] [L] [Y] [F] [I] [I] [G] [T] [F] [Q] [E] [D] [I] [Y] [C] [H] [K] [F] [I] [Q] [V] [I] [A] [L] [P] [W] [I] [A]... [M] [S] [T] [M] [Y] [N] [P] [I] [Y] [C] [C] [I] [N] [H] [R] [E] [S] [Q] [E] [R] [L] [A] [P] [R] [C]... (62)
VII

D₆
β₆
α₆
G-21
M₁
SK

D₆
β₆
α₆
G-21
M₁
SK

D₆
β₆
α₆
G-21
M₁
SK

D₆
β₆
α₆
G-21
M₁
SK

236243 5623304

9.5 —
7.5 —
4.4 —
2.4 —
1.35 —

A B C D E F G H I J K L M N O

FIG. 3

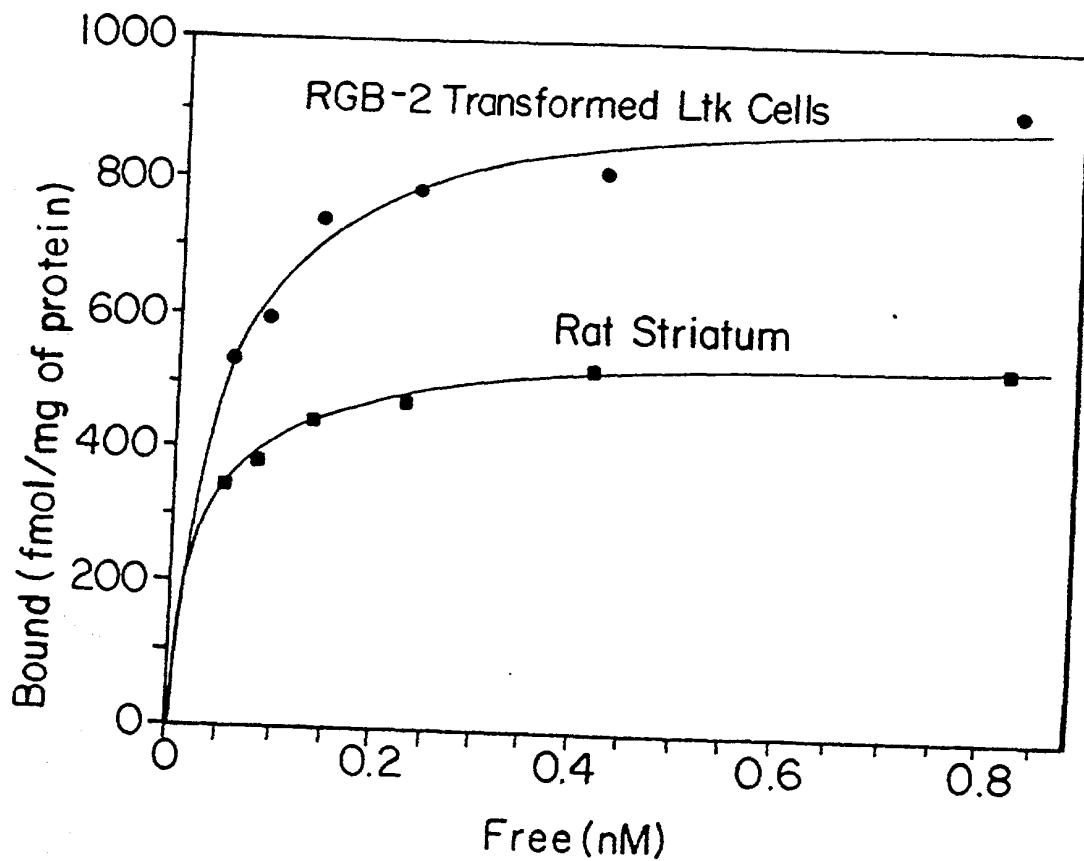


FIG. 4A-1

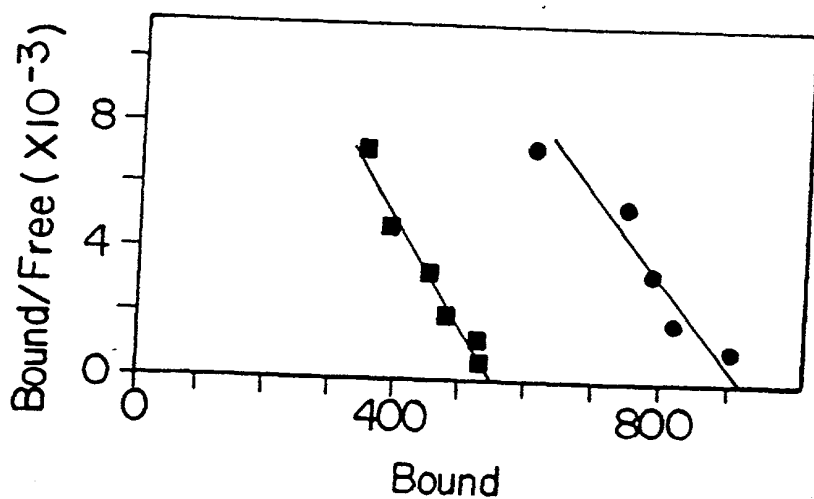
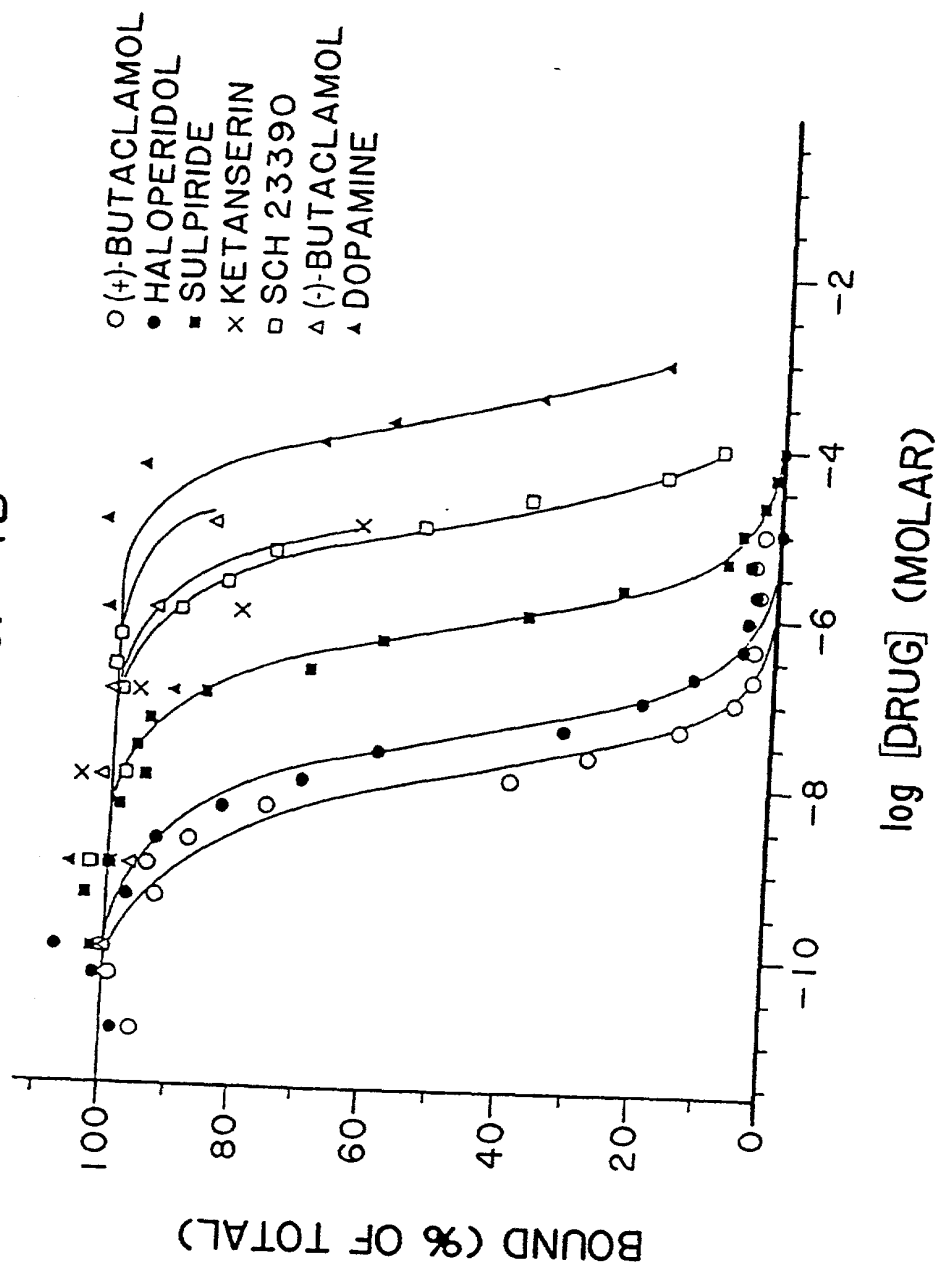


FIG. 4A-2

FIG. 4B



DRUG

Ki (nM)

RGB-2

Transformed Ltk-Cells

Rat Striatum

(+)-Butaclamol
 (-)-Butaclamol
 Haloperidol
 Dopamine + GTP
 Sulpiride
 high affinity
 low affinity
 SCH 23390
 high affinity
 low affinity
 Ketanserin
 high affinity
 low affinity

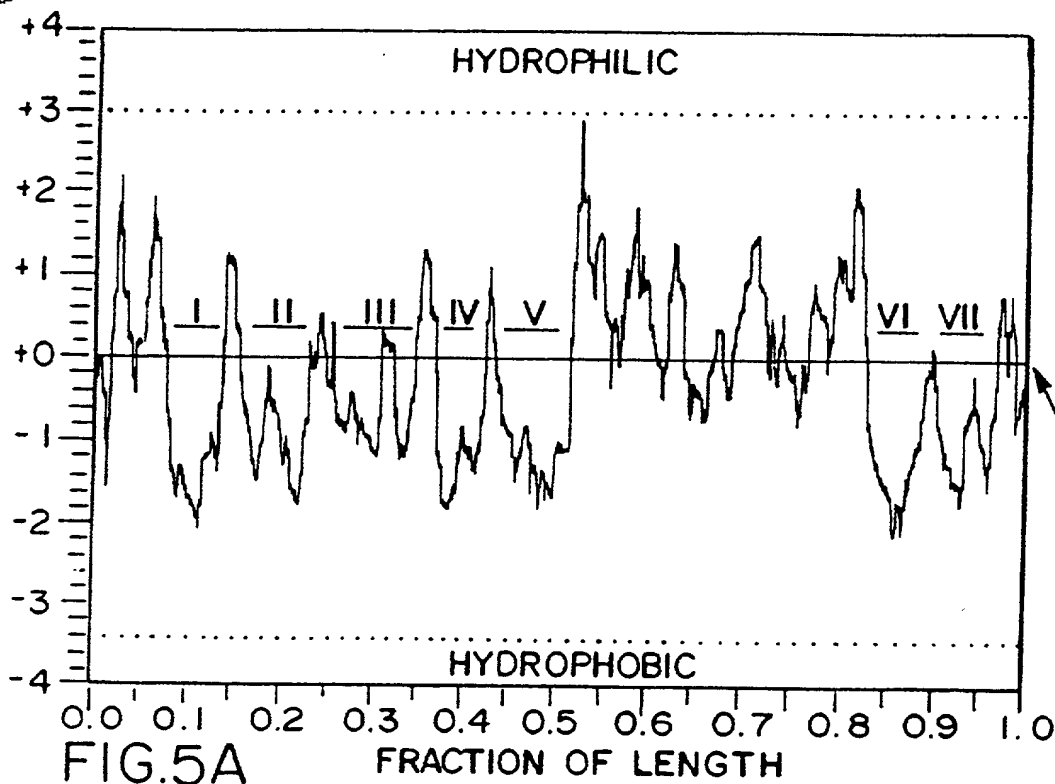
0.83
 >1,000
 3.0
 17,000
 80

 1,000

 >1,000

1.0
 >1,000
 5.3
 6,300
 67 (87%)
 >10,000 (13%)
 35 (16%)
 780 (84%)
 27 (25%)
 >1,000 (75%)

FIG. 4C



RGB-2

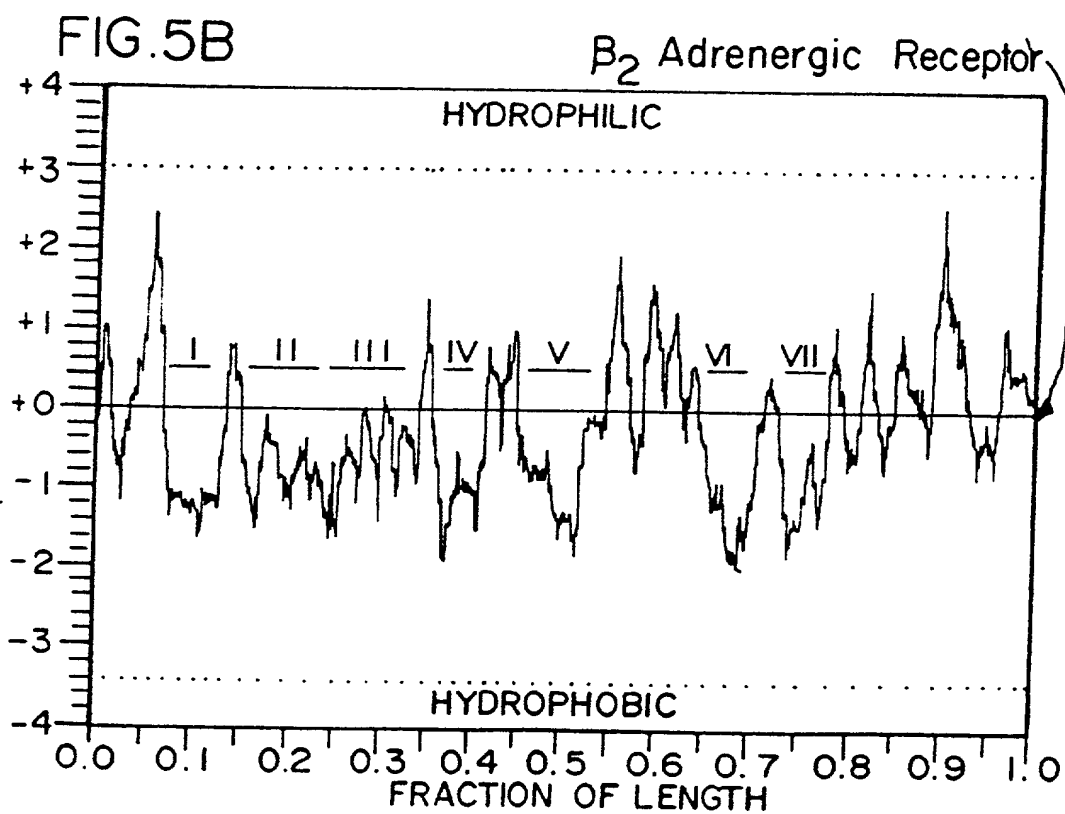
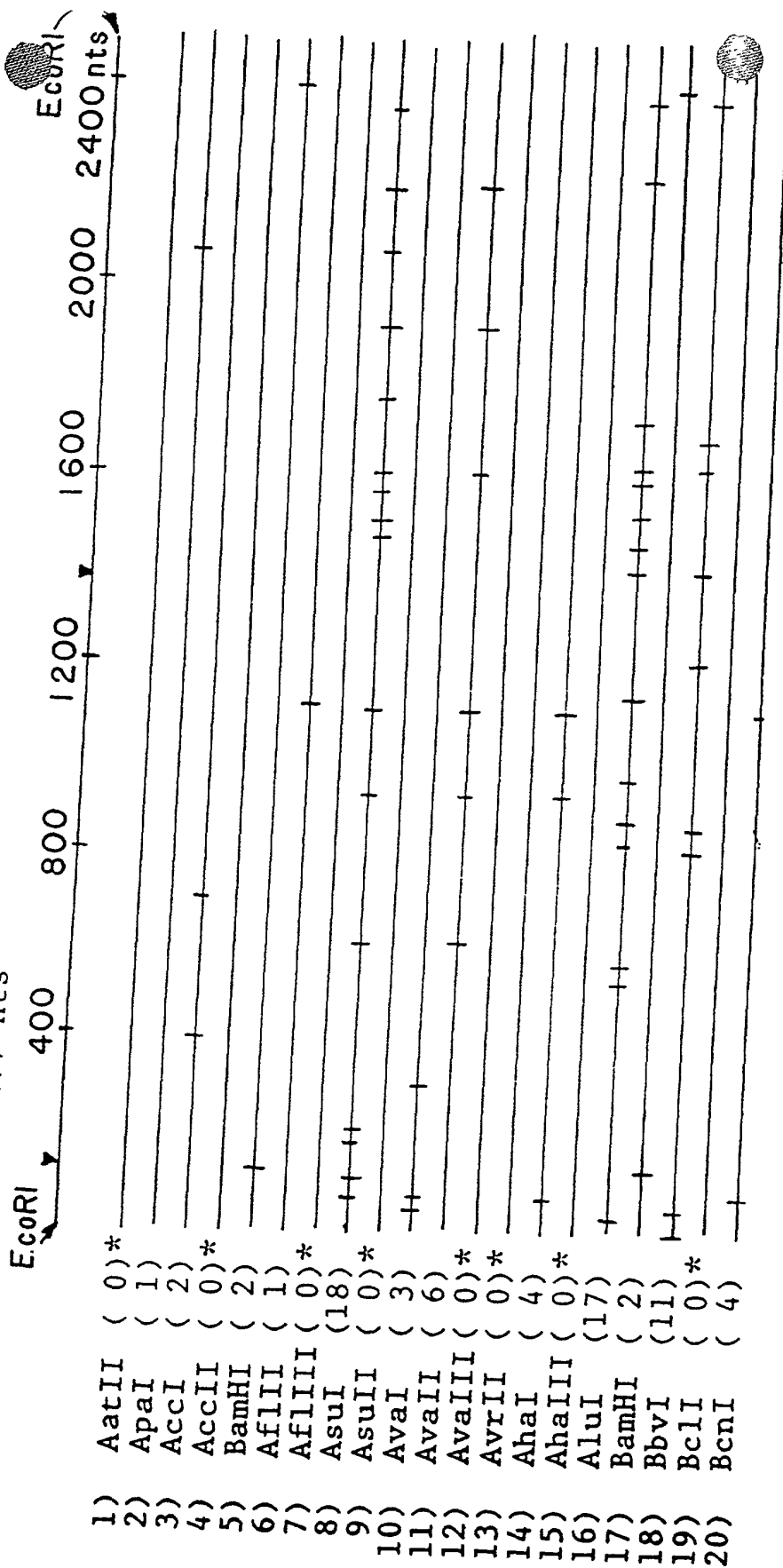


FIG. 6A

Length of DNA: 2477 nts



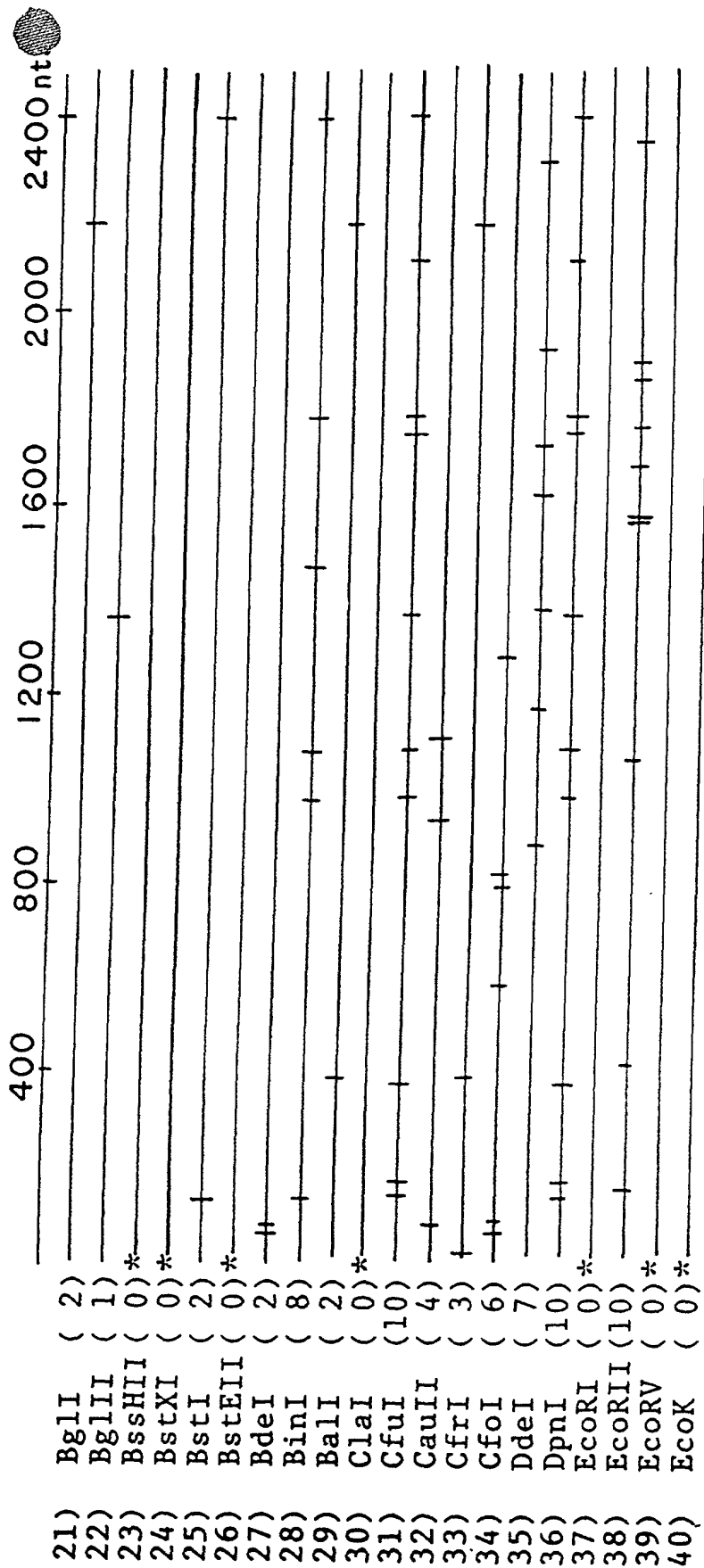


FIG. 6B

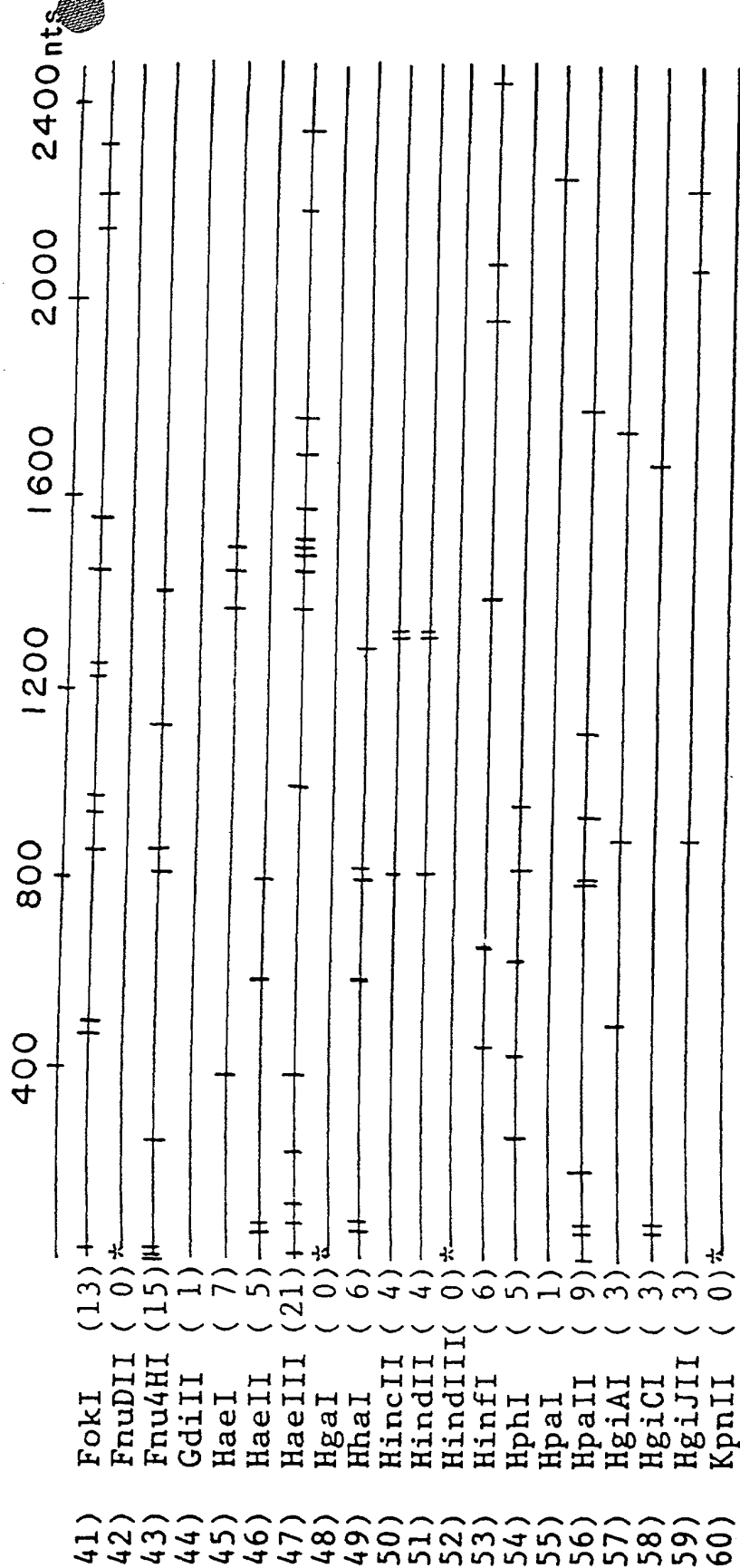


FIG. 6C

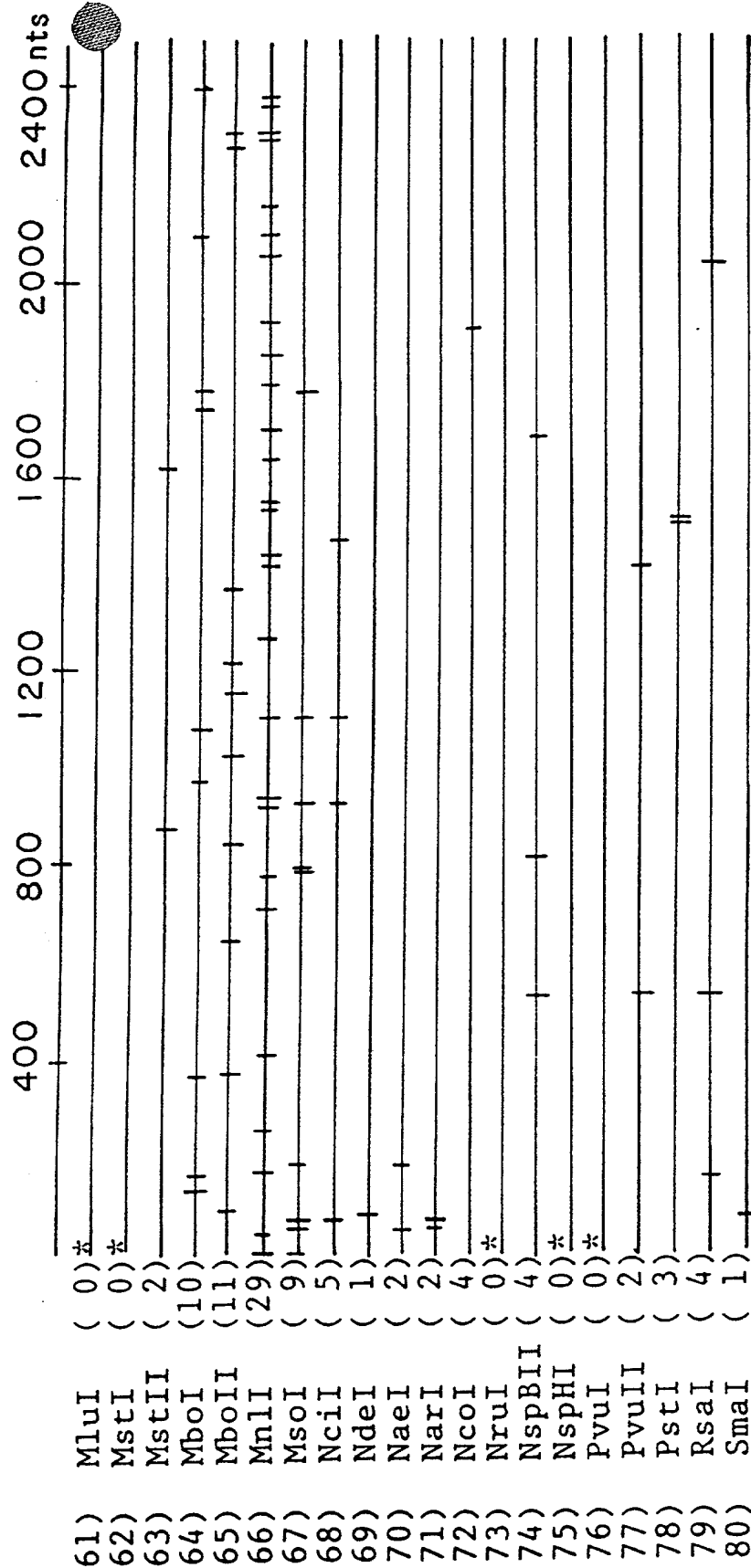


FIG. 6D

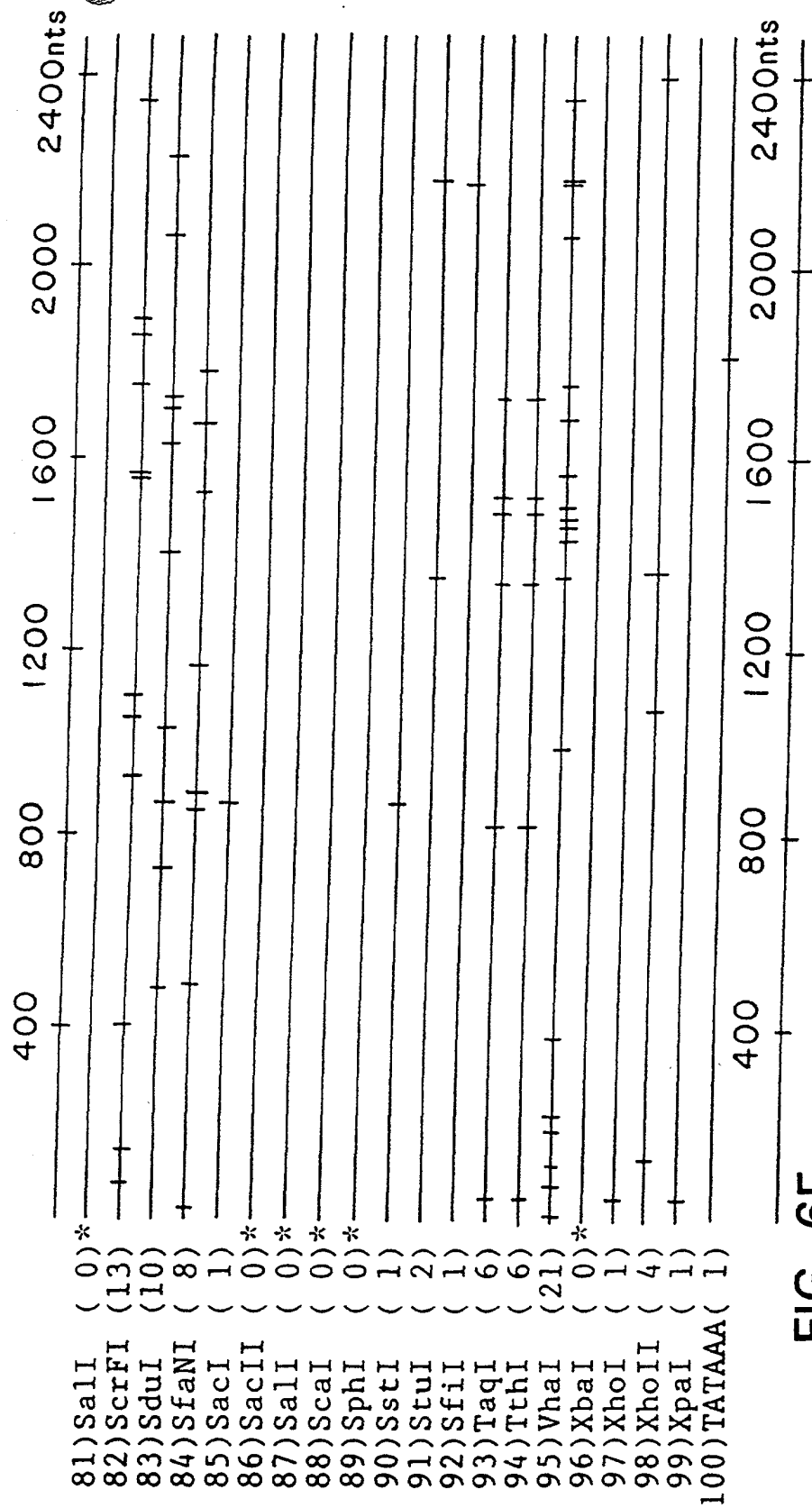


FIG. 6E

FIG. 7A

3' GTC GGG TGG GCT CTC CTG GGC CAT GTC GGG GTA GGG TGG GTC GGT GGT CGA 54
 5' CAG CCC ACC CGA GAG GAC CCG GTA CAG CCC CAT CCC ACC CAG CCA CCA GCT 3
 Gln Pro Thr Arg Glu Asp Pro Val Gln Pro His Pro Thr Gln Pro Pro Pro Ala
 Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln Leu
 Ala His Pro Arg Gly Pro Gly Thr Ala Pro Ser His Pro Ala Thr Thr Ser

81 108
 CTG AGA GGG GCT GGG CAG GGT GGT ACC AGA GGT GTC GTC AGG GCT GTC GGG GCG
 GAC TCT CCC CGA CCC GTC CCA CCA TGG TCT CCA CAG CAC TCC CGA CAG CCC CGC
 Asp Ser Pro Arg Pro Val Pro Pro Trp Ser Pro Gln His Ser Arg Gln Pro Arg
 Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala
 Leu Ser Pro Thr Arg Pro Thr MET Val Ser Thr Ala Leu Pro Thr Ala Pro Pro

135 162
 GTT TGG TCT CTT CTT ACC CGT ACC GGT TTC CTG GTG GGG TTC CTA ACG GTT CTA
 CAA ACC AGA GAA GAA TGG GCA TGC CAA AAG GAC CAC CCC AAG GAT TGC CAA GAT
 Gln Thr Arg Glu Glu Trp Ala Cys Gln Lys Asp His Pro Lys Asp Cys Gln Asp
 Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr Pro Arg Ile Ala Lys Ile
 Asn Gln Arg Arg MET Gly MET Pro Lys Gly Pro Pro Gln Gly Leu Pro Arg Ser

189 216
 GAA ACT CTA GGT CTG GTA CCG GTT ACC GTT TTG GGC CTG GAG GGA GTT CTG GTA
 CTT TGA GAT CCA GAC CAT GCC CAA TGG CAA AAC CCG GAC CTC CCT CAA GAC CAT
 Leu . Asp Pro Asp His Ala Gln Trp Gln Asn Pro Asp Leu Pro Gln Asp His
 Phe Glu Ile Gln Thr MET Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr MET

FIG. 7B

CTC GGC ATC CTT C6A G55 GGT CGT CCT CTT CTT TCG GTG AGT CTA CGA GCG 270
 GAG CCG TAG GAA G3T C44 CCA GCA GAA GGA GAA AGC CAC TCA GAT GCT CGC
 Glu Pro . Glu C TT Pro Ala Glu Gly Glu Ser His Ser Asp Ala Arg
 Ser Arg Arg Lys Leu Phe Gln Gln Lys Lys Lys Ala Thr Gln MET Leu Ala
 Ala Val Gly Ser Ser Arg Arg Arg Lys Pro Leu Arg Cys Ser Pro
 243
 GTA 5CA AGA GCC GCA CAA GTA GTA GAC CGA CGG GAA GAA GTA GTG TGT GTA 324
 CAT 4GT TCT CGG CGT GTT CAT CAT CTG CTG GCT GCC CTT CTT CAT CAC ACA CAT
 His T Ser Arg Arg Val His His Leu Leu Ala Ala Leu Leu His His Thr His
 ILE Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile
 le Phe Ser Ala Cys Ser Ser Ser Ala Gly Cys Pro Ser Ser His Thr Ser
 297
 GGA CTT GTA TGT GAC ACT GAC GAC GTT GTA GGG CGG ACA GGA CAT GTC GCG GAA GTG 378
 CCT GAA CAT ACA CTG TGA CTG CAA CAT CCC GCG TGT CCT GTC CAG CAG CTT CAC
 Pro Glu His Thr Leu . Leu Gln His Pro Ala Cys Pro Val Gln Arg Leu His
 Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr
 . Thr Tyr Thr Val Thr Ala Thr Ser Arg Leu Ser Cys Thr Ala Pro Ser Arg
 351
 CAC CGA CCC GAT ACA GTT GTC GCG GCA CTT GGG GTA GTA GAT GTG GAA GTT 432
 GTG GCT GGG CTA TGT CAA CAG CGC CGT GAA CCC CAT CAT CTA CAC CAC CTT CAA
 Val Ala Gly Leu Cys Gln Gln Arg Arg Glu Pro His His Leu His His Leu Gln
 Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn
 Gly Trp Ala MET Ser Thr Ala Pro . Thr Pro Ser Ser Thr Pro Pro Ser Thr

| | |
|---|-----|
| GTA ACT CAA GGC GTT CCG GAA GGA CTT CTA GGA GGT GAC GAC TGA GAC GAC GGA | 486 |
| CAT TGA GTT CCG CAA GGC CTT CCT GAA GAT CCT CCA CTG CTG ACT CTG CTG CCT | |
| His . Val Pro Gln Gly Leu Pro Glu Asp Pro Pro Leu Leu Thr Leu Leu Pro | |
| Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu | |
| Leu Ser Ser Ala Arg Pro Ser . Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys | |
| CGG CGT GTC GTC GGA CGA AGG GTG GAG GGA CCG GTC ACC GCC GGT CGG AGT GGG | 540 |
| GCC GCA CAG CAG CCT GCT TCC CAC CTC CCT GCC CAG TGC CGG CCA GCC TCA CCC | |
| Ala Ala Gln Gln Pro Ala Ser His Leu Pro Ala Gln Cys Arg Pro Ala Ser Pro | |
| Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro | |
| Arg Thr Ala Ala Cys Phe Pro Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu | |
| AAC GCT TGG CAC TCG TCC TCC TTC CCG ACC CAC CTA GCC GGA GGA GAT CGG GGC | 594 |
| TTG CGA ACC GTG AGC AGG AAG GCC TGG GTG GAT CGG CCT CCT CTT CTA GCC CCG | |
| Leu Arg Thr Val Ser Arg Lys Ala Trp Val Asp Arg Pro Pro Leu Leu Ala Pro | |
| Cys Glu Pro . Ala Gly Arg Pro Gly Trp Ile Gly Leu Leu Phe . Pro Arg | |
| Ala Asn Arg Glu Gln Glu Gly Leu Gly Ser Ala Ser Ser Ser Ser Pro Gly | |

FIG. 7C

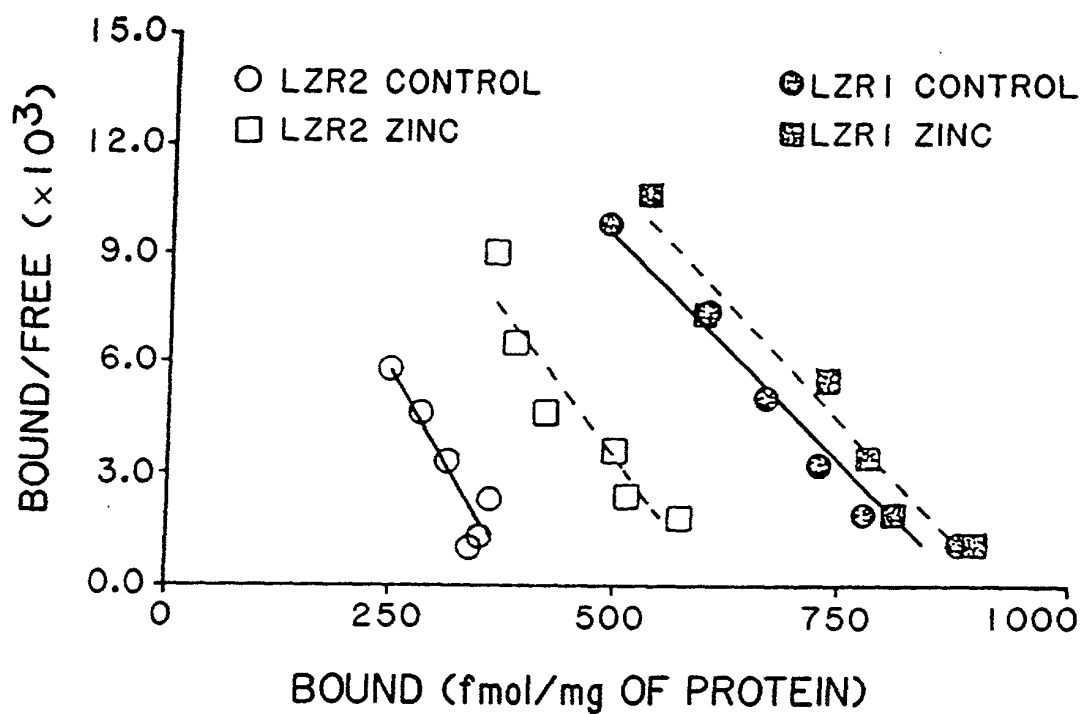


FIG. 8

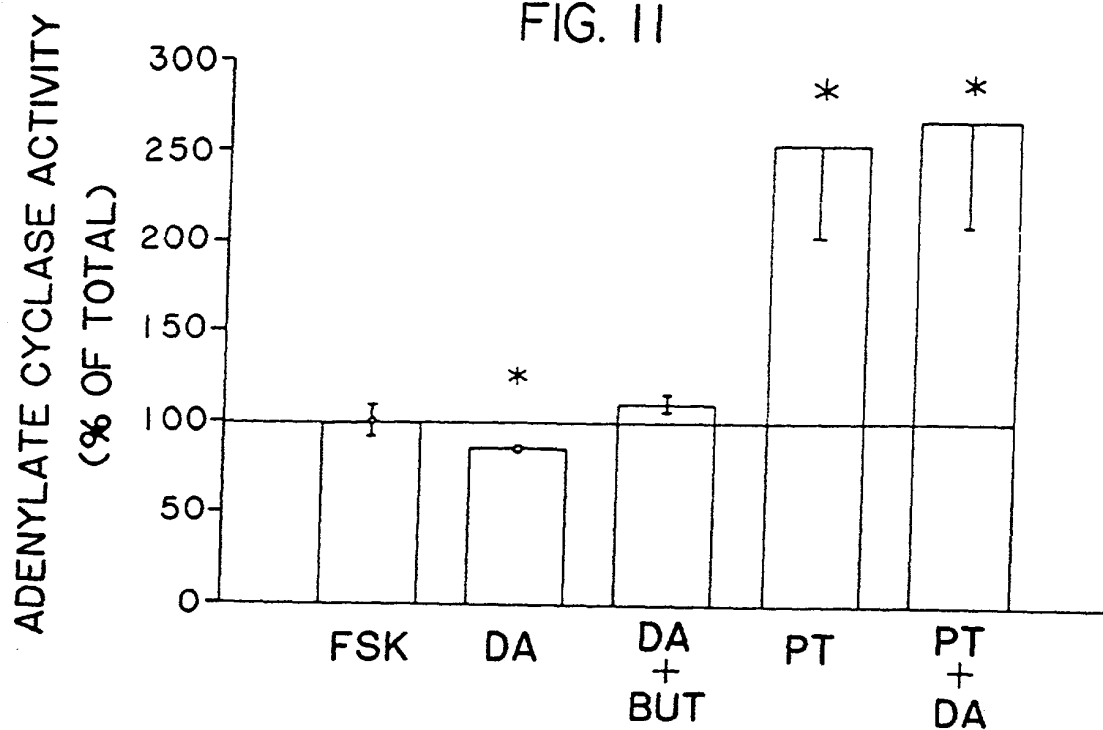


FIG. 9A

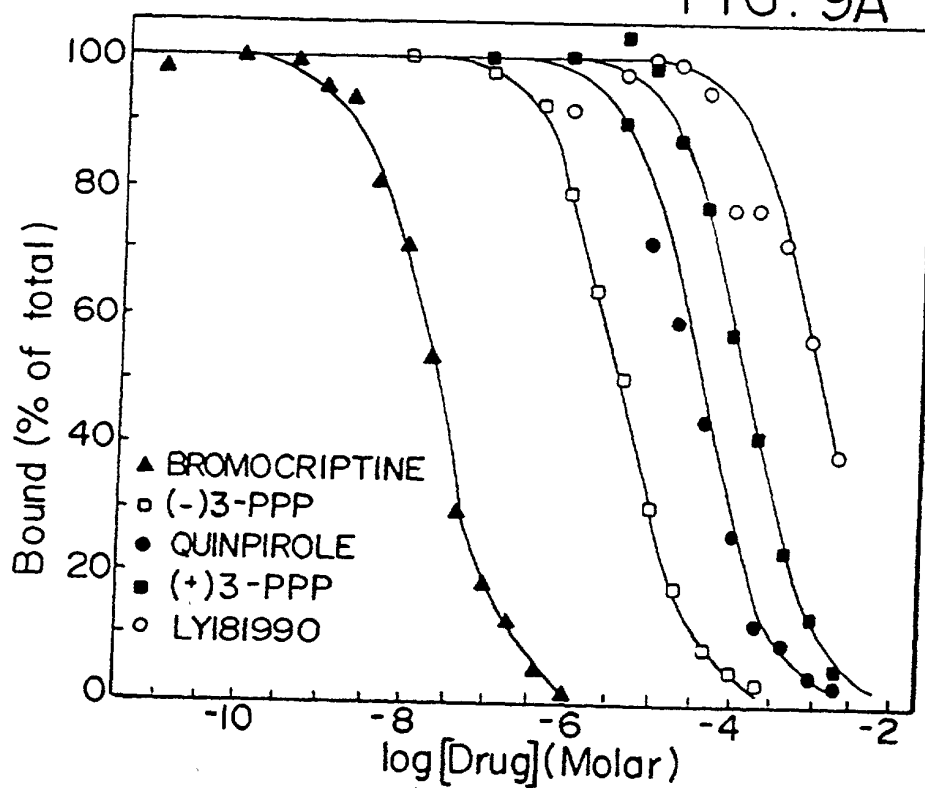
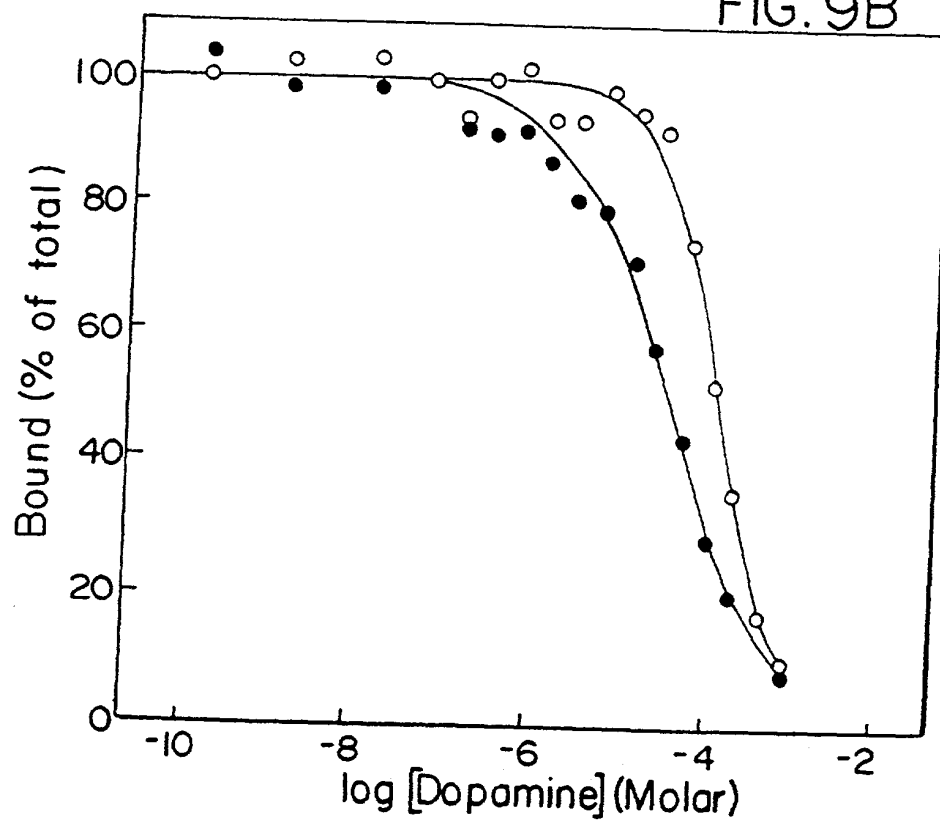


FIG. 9B



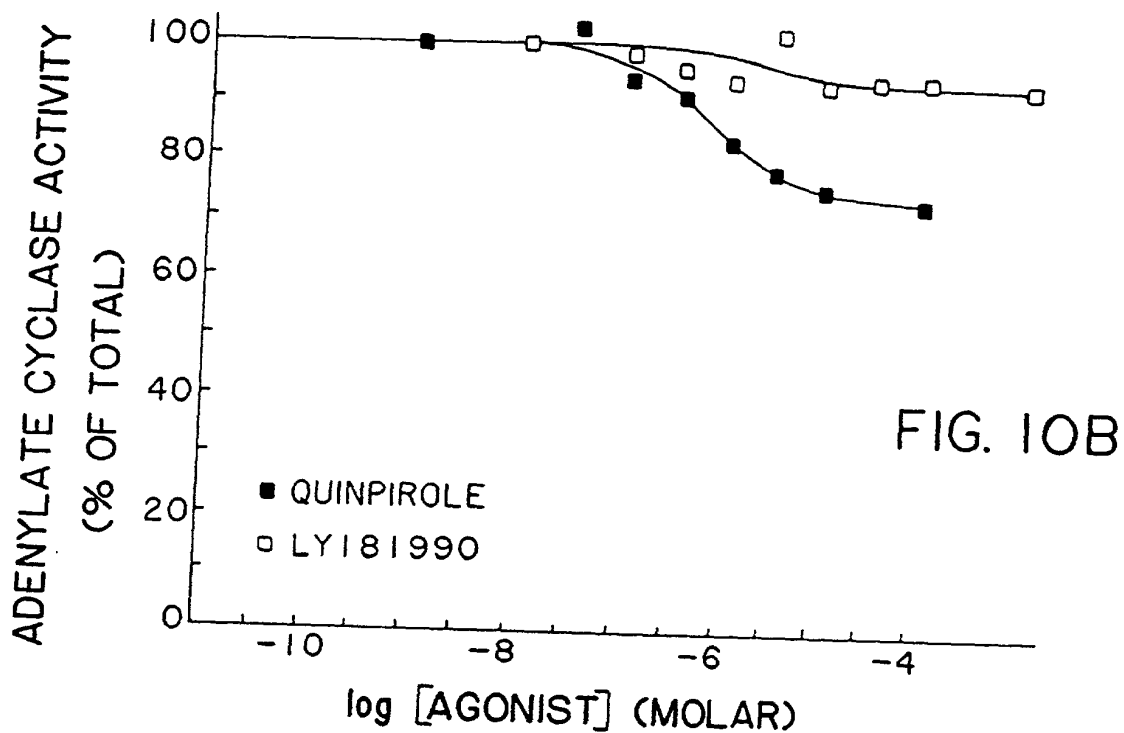
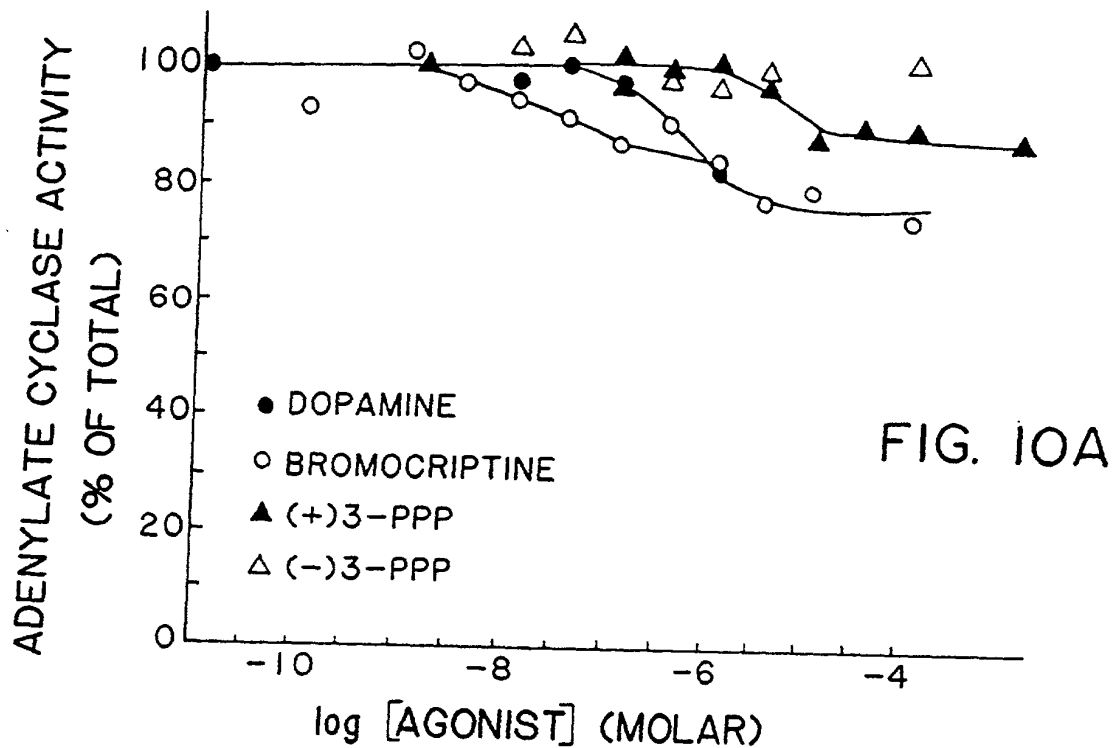


FIG. 12A

| CONTROL | | | | +P.T. | | | |
|---------|------|--------|--|-------|------|--------|--|
| BASAL | FSK | FSK+DA | | BASAL | FSK | FSK+DA | |
| 2.1 | 22.6 | 14.3 | | 1.7 | 26.7 | 23.1 | |
| 0.2 | 2.2 | 2.1 | | 0.4 | 2.0 | 0.5 | |
| — | — | 41% | | — | — | 14% | |

FIG. 12B

| CONTROL | | | | +P.T. | | | |
|---------|------|------|--------|-------|------|------|--------|
| BASAL | VIP | DA | VIP+DA | BASAL | VIP | DA | VIP+DA |
| 0.60 | 2.41 | 0.32 | 0.84 | 0.61 | 2.68 | 0.55 | 2.56 |
| 0.02 | 0.31 | 0.02 | 0.13 | 0.09 | 0.08 | 0.03 | 0.25 |
| — | — | 53% | 71% | — | — | 10% | 3% |

FIG. 12C

| CONTROL | | | | +P.T. | | | |
|---------|-----|------|--------|-------|------|------|--------|
| BASAL | VIP | DA | VIP+DA | BASAL | VIP | DA | VIP+DA |
| 0.78 | 5.1 | 0.25 | 0.76 | 0.64 | 5.29 | 0.66 | 4.76 |
| 0.04 | 0.4 | 0.03 | 0.01 | 0.01 | 0.44 | 0.03 | 0.16 |
| — | — | 68% | 88% | — | — | 0% | 12% |

| Sample | Relative Intensity (approx.) |
|----------|------------------------------|
| GH4 | 0.24 |
| GH4ZR7 | 3.0 |
| GH4ZR7Zn | 7.5 |
| GH4ZD10 | 9.5 |

FIG. 13A

FIG. 13B-1

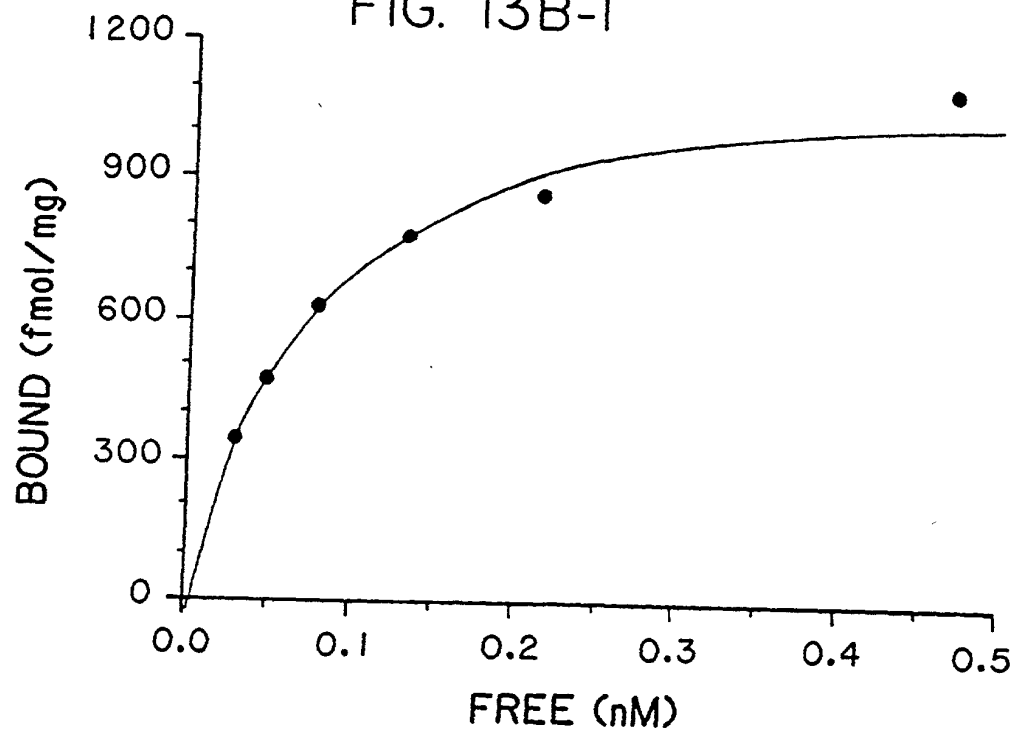
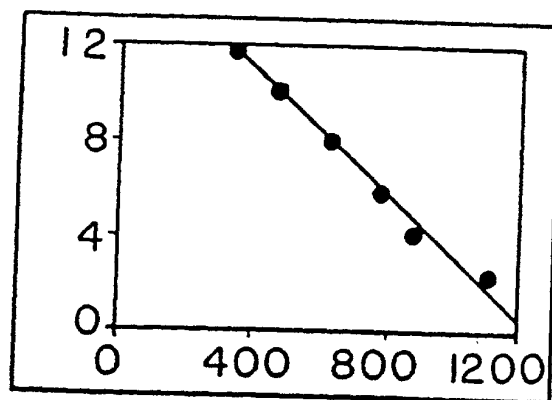
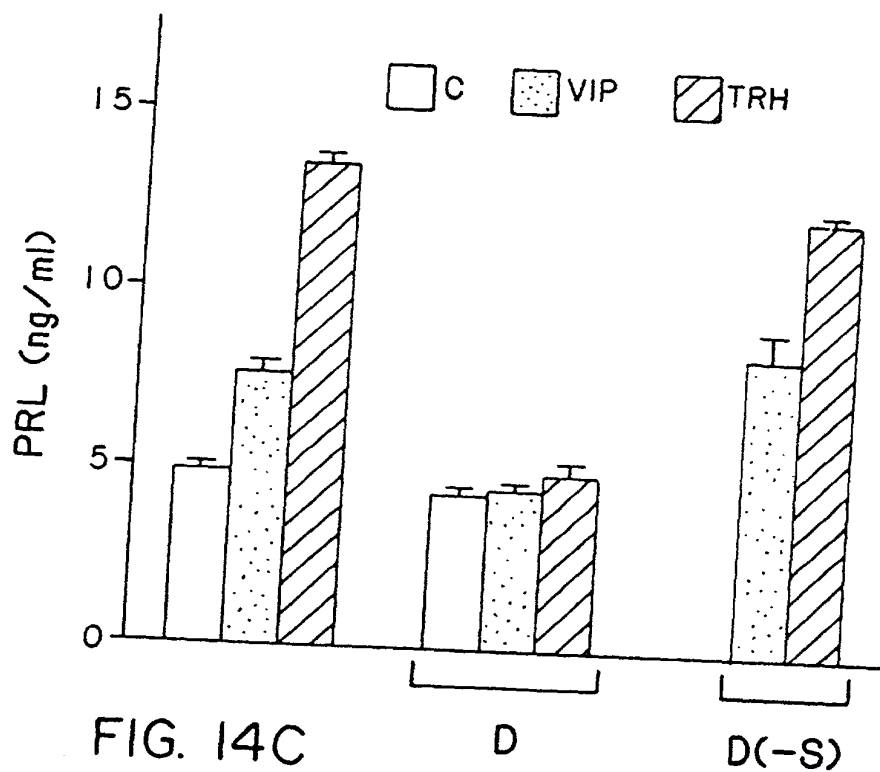
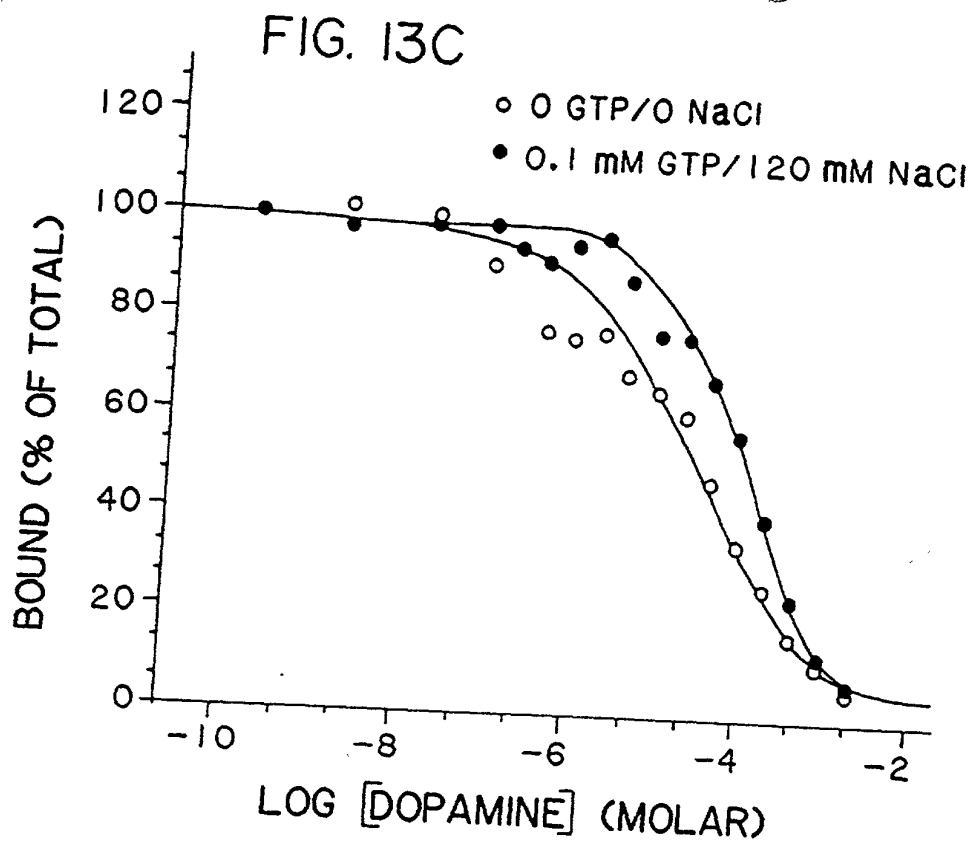


FIG. 13B-2





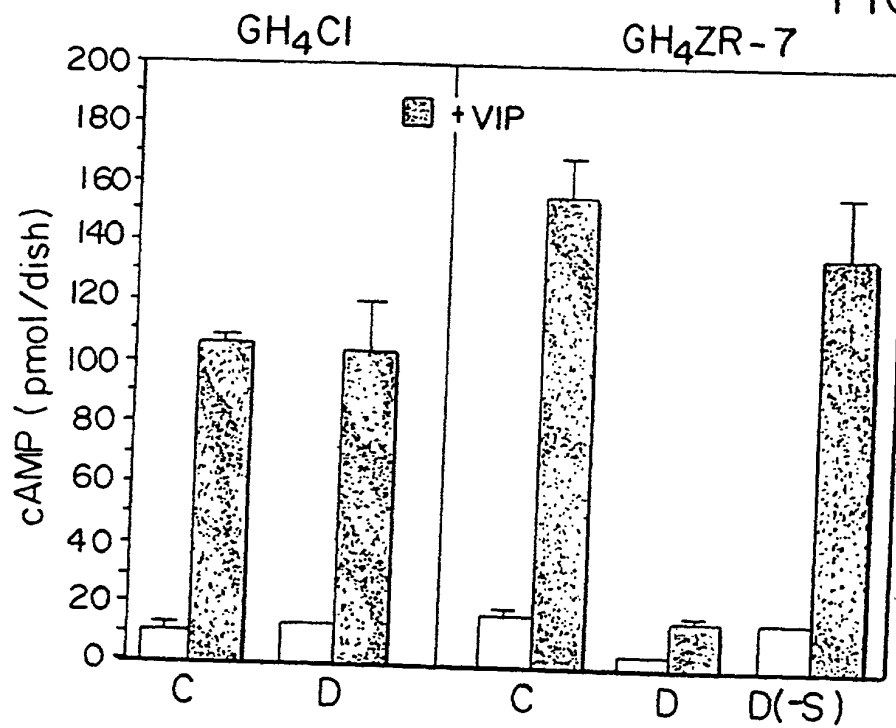
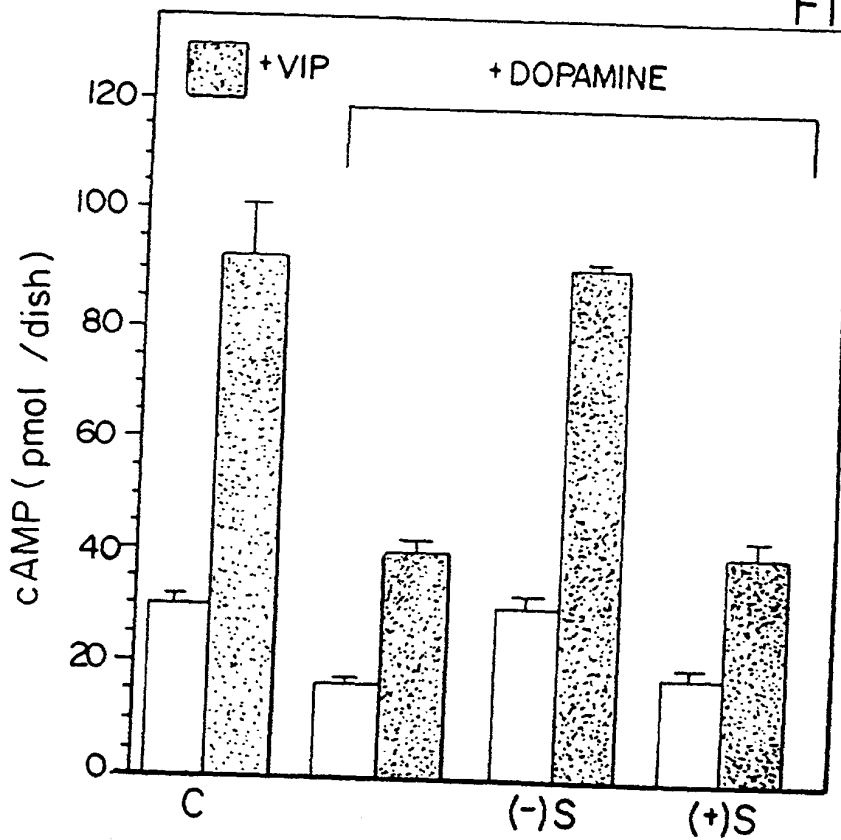
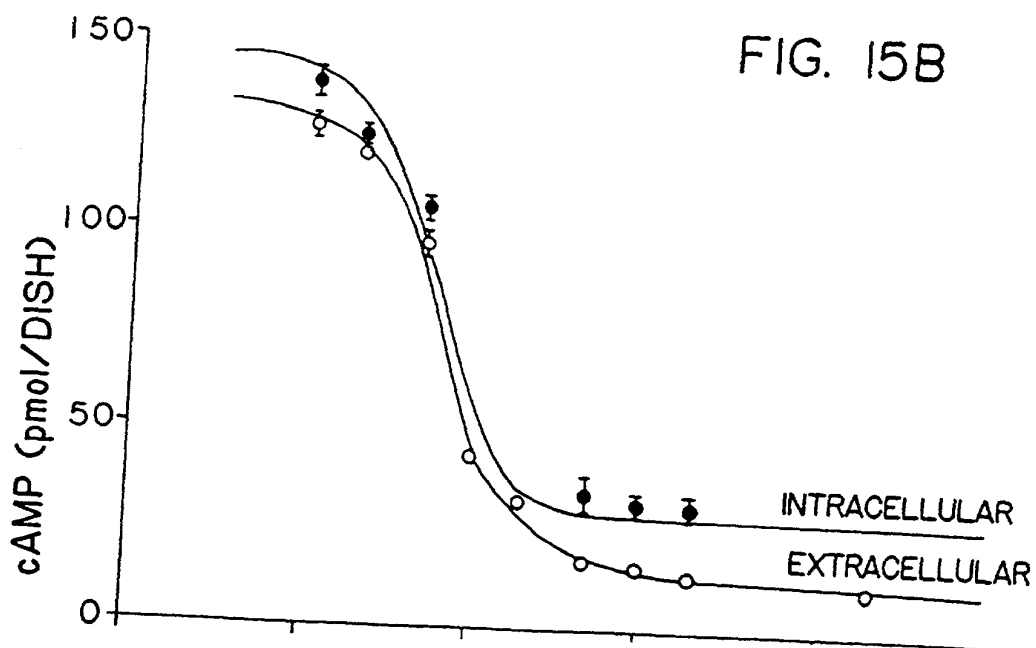
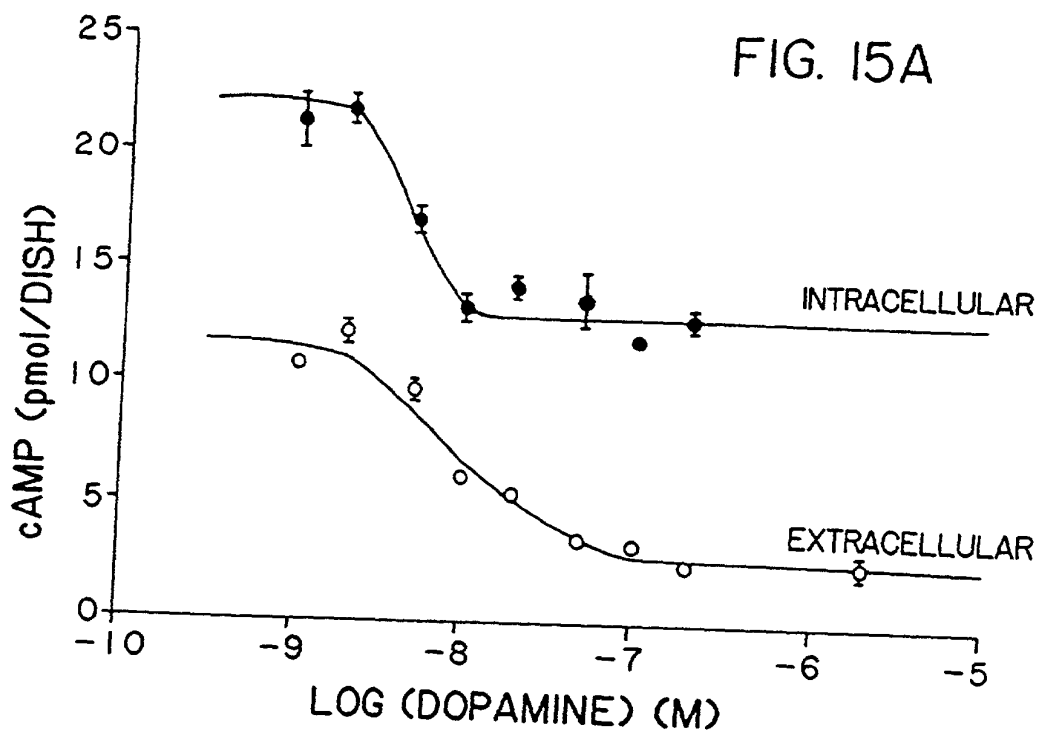
[illegible]

FIG. 14B



205270" 56403007



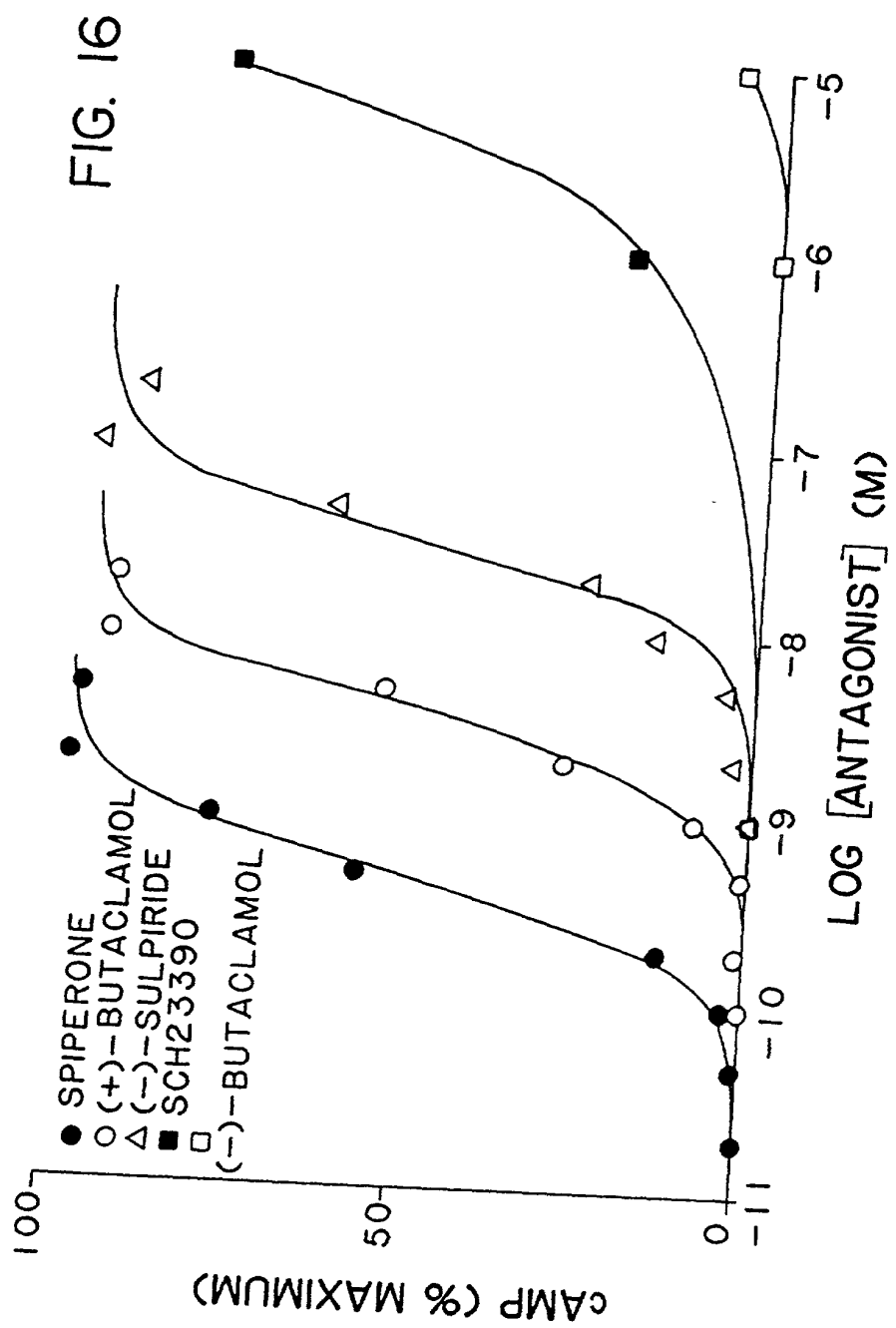


FIG.17A

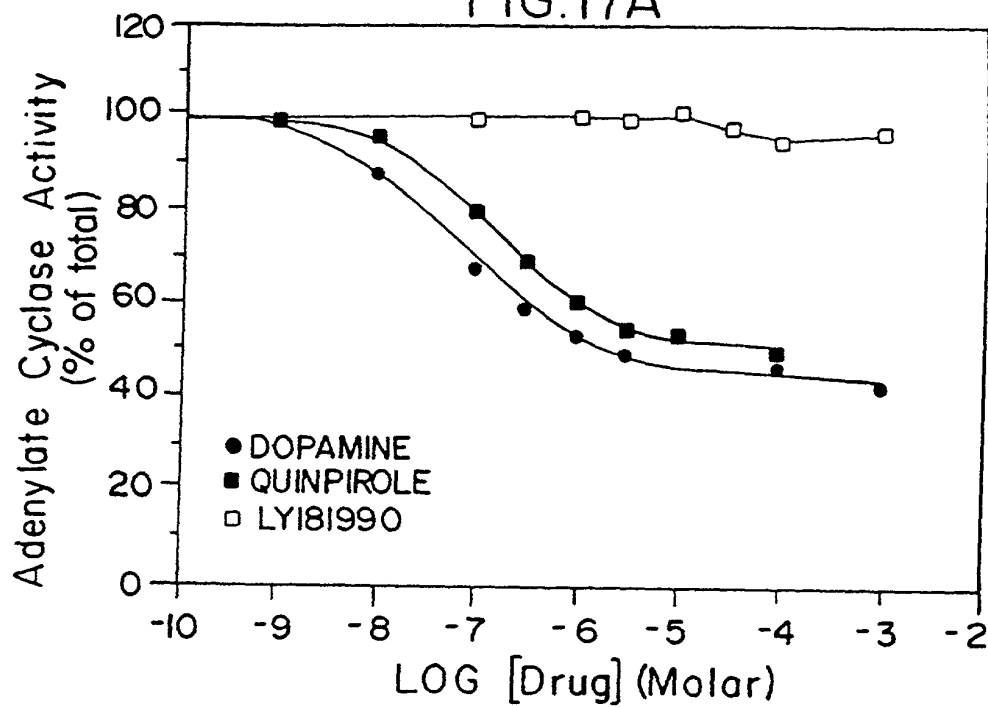
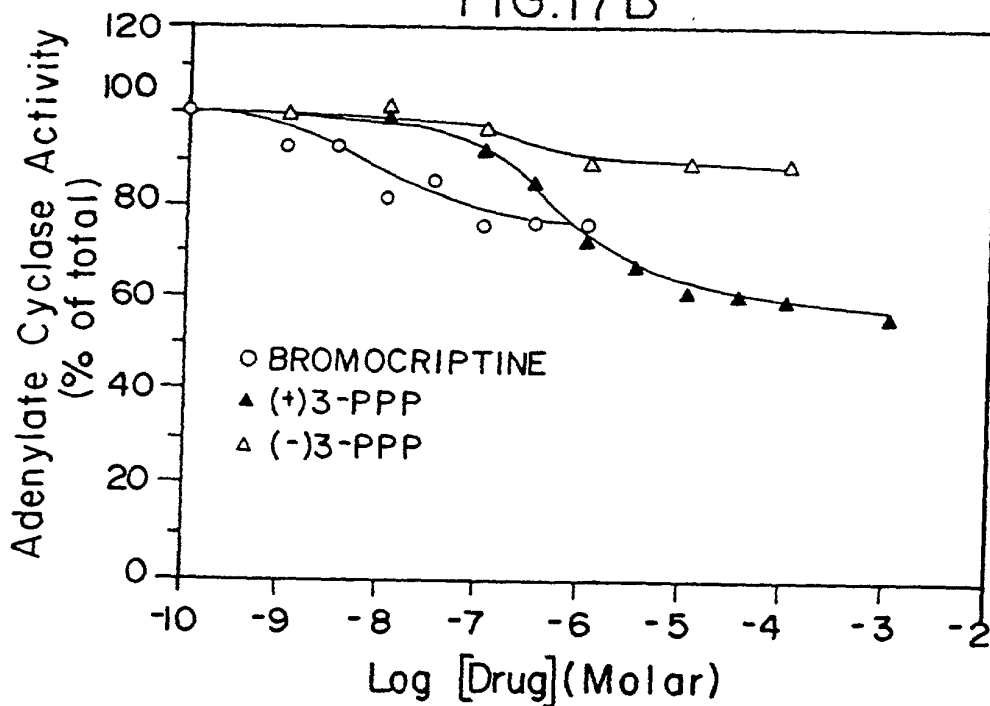


FIG.17B




```

-33 AGAGCCTGGCCACCCAGTGGCTCCACCGCCCTG
      *
METAspProLeuAsnLeuSerTrpTyrAspAspLeuGluArgGlnAsnTrpSerArg      20
      *
ATGGATCCACTGAATCTGTCTGGTATGATCTGGAGAGGCAGAACTGGAGCCCG
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
ATGGATCCACTGAACCTGTCTGGTACGATGACGATCTGGAGAGGCAGAACTGGAGCCCG
      *
ProPheAsnGlySerAspGlyLysAlaAspArgProHisTyrAsnTyrTyrAlaThrLeu      40
      *
CCCTTCAACGGGTCAGACGGGAAGCGGCAGACCCCACTACAACTACTATGCCACACTG
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
CCCTTCAATGGGTCAGAAAGGGAAGGCAGACAGGCCCACTACAACTACTATGCCATGCTG
      Glu
MET
120

```

FIG. 18A

| | | |
|---|----|-----|
| | 50 | 60 |
| LeuThrLeuLeuIleAlaValIleValPheGlyAsnValLeuValCysMETAlaValSer | | |
| CTCACCCCTGCTCATCGCTGTCTTCGGCAACGTGCTGGTGTGCATGGCTGTGTCC | | |
| | | |
| CTCACCCCTCCTCATCTTTATCATCGTCTTTGGCAATGTGCTGGTGTGCATGGCTGTATCC | | |
| PheIle | | |
| 70 | | 80 |
| ArgGluLysAlaLeuGlnThrThrThrAsnTyrLeuIleValSerLeuAlaValAlaAsp | | |
| CGGAGAGGCGCTGCAGACCAACCACTACCTGATCGTCAGCCTCGCAGTGGCCGAC | | |
| | | |
| CGAGAGAGGCTTTCAGACCAACCACTACTGATAGTCAGCCTTGCCTGTGGCTGAT | | |
| | | 240 |

| | |
|---|-----|
| 90 | 100 |
| LeuLeuValAlaThrLeuValMETProTrpValValTyrLeuGluValValGlyGluTrp | |
| CTCCTCGTCCGCACACTGGTCAATGCCCTGGGTTGTCTACCTGGAGGTGGTAGGTGAGTGG | |
| | |
| CTTCTGGTCCGCACACTGGTAATGCCCTGGGTTGTCTACCTGGAGGTGGTGGTGGTGGTGG | |

FIG. 18B

[illegible]

SerIleLeuAsnLeuCysAlaIleSerIle AspArgTyrThrAlaValAlaMetProMet
 130 140
 AGCATCCTGAACCTTGTGCTGCATCAGCATCGACAGGTACACAGCTGTGCCATGCCCATG
 IIIIIIIIIII IIIIIIIIIII IIIIIIIIIII IIIIIIIIIII IIIIIIIIIII
 AGCATCCTGAACCTTGTGCTGCATCAGCATCGACAGGTACACAGCTGTGCCAATGCCCATG

| | | | |
|---------------------------------------|-----|------------------------------------|-----|
| LeuTyrAsnThrArgTyrSerSerLysArgArg | 150 | <u>ValThrValMETIleSerIleValTrp</u> | 160 |
| CTGTACAATACGCGCTACAGCTCCAAGCGCCGGGTCA | | CCGTCATGATCTCCATCGTCTGG | |
| IIIIII II II IIIIIIIIIIIIIIIIIIIIIII | | II II IIIIIIIIIII IIII IIIIIII | 480 |
| CTGTATAACACACGCTACAGCTCCAAGCGCCGAGTT | | ACTGTGTCATGATTGCCATTGTCTGG | |

Ala

FIG. 18C

IV

ValLeuSerPheThrIleSerCysProLeuLeuPheGlyLeuAsnAsnAlaAspGlnAsn 170 180
 GTCCTGTCCTTCACCATCTCCTGCCCACTCCTCTTCGGACTCAATAACGCAGACCAGAAC
 !!!
 GTCCTGTCCTTCACCATCTCCTGCCCACTGCTCTTCGGACTCAACAATACAGACCAGAAT
 Thr

GluCysIleIleAlaAsnProAlaPheValValTyrSerSerIleValSerPheTyrVal 190 200
 GAGTGCATCATCGCCAAACCGGCTTCGTGGTCTACTCCTCCATCGTCTCCTTCTACGTG
 !!!!! !!!!!!!!!!!!! !!!!! !!!!!!!!!!!!!!!!!!!!!!!!! !!!!! !!!!!!!!!
 GAGTGATCATCGCCAAACCGCTTGTGGTCTACTCCTCCATTGTCTCATTTCTACGTG 600

ProPheIleValThrLeuLeuValTyrIleLysIleTyrIleValLeuArgArgArg 210 220
 CCCTTCATTGTCACCCCTGCTGGTCTACATCAAGATCTACATTGTCTCCTCCGCAGACGCCGC
 !!!!! !!!!! !!!!!!!!!!!!! !!!!! !!!!!!!!!!!!!!!!! !!!!! !!!!!
 CCCTTCATCGTCACTCTGCTGGTCTATATCAAAATCTACATCGTCTCCTCCGGAAGCCCGG
 Lys

FIG. 18D

| | | |
|---|-----|--------|
| LysArgValAsnThrLysArgSerArgAlaPheArgAlaHisLeuArgAlaProLeu | 230 | 240 |
| AAGCGAGTCAACACCAACGACGACCGAGCTTTCAGGGCCACCTGAGGGCTCCACTA | | |
| | | 720 |
| AAGCGGTCAACACCAAGCGCAGCAGTCGAGCTTTCAGAGCCCAACCTGAAGACACCACTC | | |
| | Asn | LysThr |
| | | |
| | 250 | * |
| LysGlyAsnCysThrHisProGluAspMETLysLeuCysThrValIleMETLysSerAsn | | |
| ▼ AAGGGCAACTGTACTCACCCCGAGGACATGAACTCTGCACCGTTATCATGAAGTCTAAT | | |
| !!! | | |
| AAG..... | | |
| | 270 | 280 |
| GlySerPheProValAsnArgArgArgValGluAlaAlaArgArgAlaGlnGluLeuGlu | | |
| GGGAGTTTCCACAGTGAACAGCGCGAGAGTGGAGGCTGCCCGCGAGCCAGAGCTGGAG | | |
| | | |
|GATGCTGCCCGCGAGCTCAGGAGCTGGAA | | 840 |
| | Asp | |

FIG. 18E

| | | |
|---|-----|-----|
| METGluMETLeuSerSerThrSerProProGluArgThrArgTyrSerProIleProPro | 290 | 300 |
| ATGGAGATGCTCTCCAGCACCAAGCCCAAGAGAGAGACCCGGTACAGCCCATCCACCC | | |
| IIIIIIIIII II IIIIIIIIIII II IIIIIIIIIII IIIIIIIIIII III | | |
| ATGGAGATGCTGTCAAGCACCAAGCCCAAGAGAGAGACCCGGTATAGCCCATCCCTCCC | | |
| SerHisHisGlnLeuThrLeuProAspProSerHisHisGlyLeuHisSerThrProAsp | 310 | 320 |
| AGCCACCAACGCTGACTCTCCCCGACCCGTCACCATGCTCTCCACAGCACTCCCGAC | | |
| II IIIIIIIIIII IIIIIIIII II II IIIIIIIII II II IIIII III | | 960 |
| AGTCACCAACGCTCACTCTCCCTGATCCATCCACCAAGGCTACATAGCAACCTGAC | | Asn |
| SerProAlaLysProGluLysAsnGlyHisAlaLys AspHisProLysIleAlaLys | 330 | 339 |
| AGCCCCGCCAAACCAAGAGAAGATGGGCATGCCAAA...GACCAACCCCAAGATTGCCAAG | | |
| II II IIIIIIIIIIIIIIIIIIIII IIIII II II IIIII IIIIIIIIIII | | |
| AGTCCTGCCAAACCAAGAGAAGATGGGCACGCCCAAGATTGTCAATCCAGGATTGCCAAG | | |
| IleValAsn Arg | | |

FIG. 18F

IlePheGluIleGlnThrMETProAsnGlyLysThrArgThrSerLeuLysThrMETSer
 ATCTTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGACCTCCCTCAAGACCATGAGC
 TTTCTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGACCTCCCTTAAGACCATGAGC
 Phe

ArgArgLysLeuSerGlnGlnLysGluLysLysAlaThrGlnMETLeuAlaIleValLeu

CGTAGGAAGCTCTCCACGAGAAGGAGAAGAAAGCCACTCAGATGCTCGCCATTGTTCTC
II II IIIIII IIIIII IIIIII IIIIII IIIIII IIIIII IIIIII IIIIII
CGCAGAAAGCTCTCCACGAGAAGGAGAAGAAAGCCACTCAGATGCTTGCCATTGTTCTC

VI

| | | |
|--|-----|------|
| GlyValPheIleIleCysTrp0LeuProPhePheIleThrHisIleLeuAsnIleHisCys | 389 | 399 |
| ▼ | | |
| GGCGTGTTCATCATCTGGCTGGCTGCCCTTCTTTCATCACACACATCCTGAACATACACTGT | | |
| II III | | 1197 |
| GCCGTCAACCCCATCATCTACACCACCTTCAACATCGAGTTCGCAAGGCCTTCATGAAG | | |
| | | MET |

FIG. 18G

AspCysAsnIleProProValLeuTyrSerAlaPheThrTrpLeuGlyTyrValAsnSer
 409 VII 419

GACTGCAACATCCCGCCTGTCTGTACAGCGCCTTACCGTGGCTGGGCTATGTCAACAGC
 II IIIIIIIIIII II IIIII IIIIIIIIIII IIIIIIIIIIIII IIIII
 GATTGCAACATCCCAACAGTCCTCTACAGCGCCTTACATGGCTGGGCTATGTCAACAGT

AlaValAsnProIleIleTyrThrThrPheAsnIleGluPheArgLysAlaPheLeuLys
 429 439

GCCGTGAACCCCATCATCTACACCACTTCAACATTGAGTTCCGCAAGGCCTTCCTGAAG
 IIIII IIIIIIIIIII IIIIIIIIIII IIIII IIIIIIIIIII IIIII 1317
 GCCGTCAACCCCATCATCTACACCACTTCAACATCGAGTTCCGCAAGGCCTTCATGAAG
 IleLeuHisCys * MET

ATCCTCCACTGCTGACTCTGCTGCTGCCCGGCACAGCAGCCTGCTTCCCACCTCCCTGCC
 III I IIIIIIIII
 ATCTTGCACTGCTGA

FIG. 18H

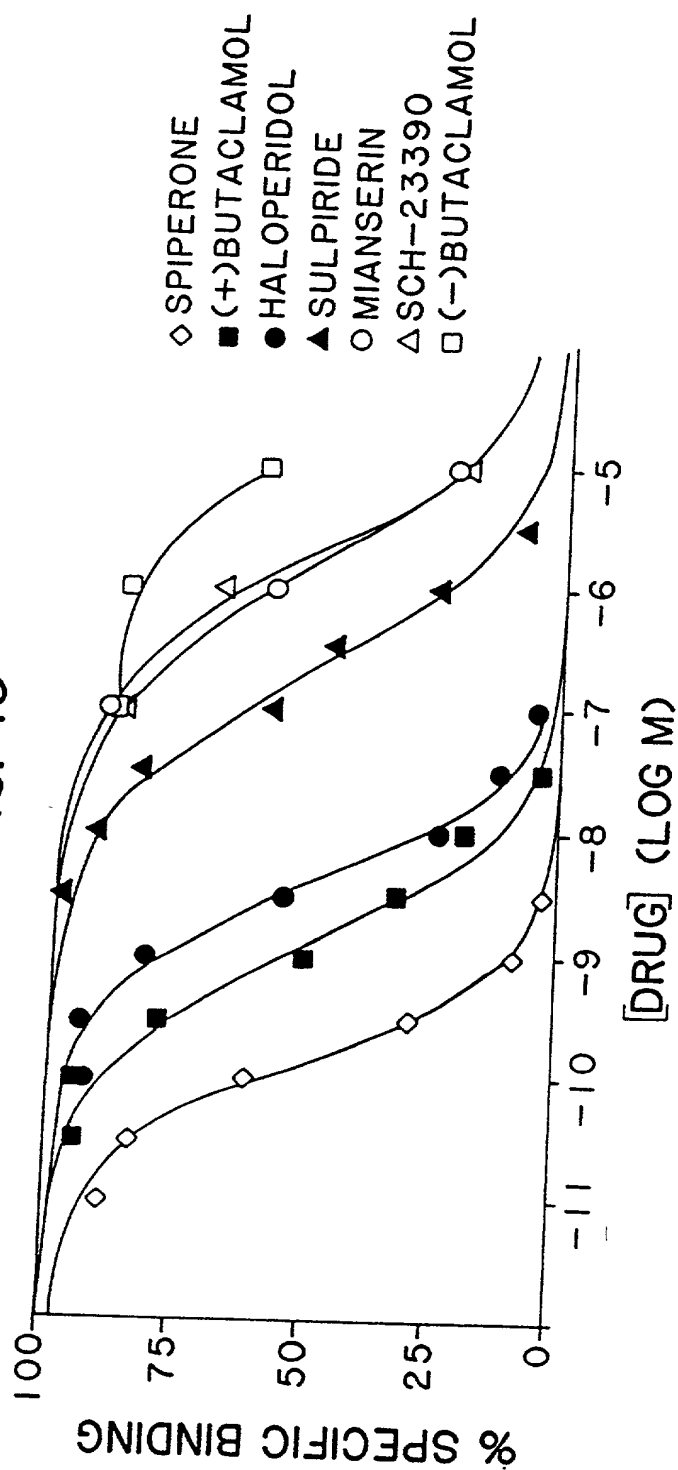
CAGGCCGGCCAGCCTCACCCCTTGCGAACCGTGAGCAGGAAGGCTGGGTGGAICGGCCTC 1437
 CTCCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTTCGCTTGGCTCCATGCTCCTCACTGCCCG
 CACACCCTCACTCTGCCAGGCGAGTGCTAGTGAGCTGGGCATGGTACCAGCCCTGGGGCT 1557
 GGCCCCAGCTCAGGGCAGCTCATAGAGTCCCCCTCCACCTCCAGTCCCCCTATCCTT
 GGCAACCAAGATGCAGCCGCCTTCCTTGACCTTCCTCTGGGGCTCTAGGGTTGCTGGAGC 1677
 CTGAGTCAGGGCCAGAGGCTGAGTTTCTCTTTGTGGGGCTTGGCGTGGAGCAGGCGGT
 GGGGAGAGATGGACAGTTCACACCCCTGCAAGGCCACAGGAGGCAAGCAAGCTCTCTTGC 1797
 CGAGGAGCCAGGCAACTTCAGTCTCTGGGAGACCCATGTAAATACCAGACTGCAGGTTGGA
 CCCCAAGGATTCCCAAGCCAAAACCTTAGCTCCCTCCCGCACCCCGATGTGGACCTCTA 1917

FIG. 18I

CTTCCAGGCTAGTCCGGACCCACCTACCCCGTTACAGCTCCCAAGTGTTCCACAT
 GCTCTGAGAAGAGAGCCCTCATCTTAAGGGCCCAGGAGGTCTATGGGAGAGGAACT 2037
 CCTTGGCCTAGCCCACCCCTGCTGCCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC
 ACATGCTGGCCAGCCCTGGGGCCTGGCAGGAGGTGAGGCCCTGGAACCTCTATCTGGGCCT 2157
 GGGCTAGGACATCAGAGGTTCTTTGAGGACTGCCCTCTGCCACACTCTGACGCAAAACC
 ACTTTCCTTTCTATTCTTCTTCTGGCCTTTCCCTCTCTCCTGTTTCCCTTCCCTTCCACTGC 2277
 CTCTGCCCTTAGAGGAGCCACGGCTAAGAGGCTGCTGAAACCATCTGGCCTGGCCTGGC
 CCTGCCCTGAGGAAGGAGGGCAAGCTGCAGCTTGGGAGAGCCCCTGGGGCCTAGACTCTG 2397
 TAACATCACTATCCGATGCCACCAAACTAATAAACTTTGACGAGTCACCTTC (A)_n 2449

FIG. 18J

FIG. 19



200270-562333

1 2 3 4

kb

—12.0

— 6.0

— 4.0

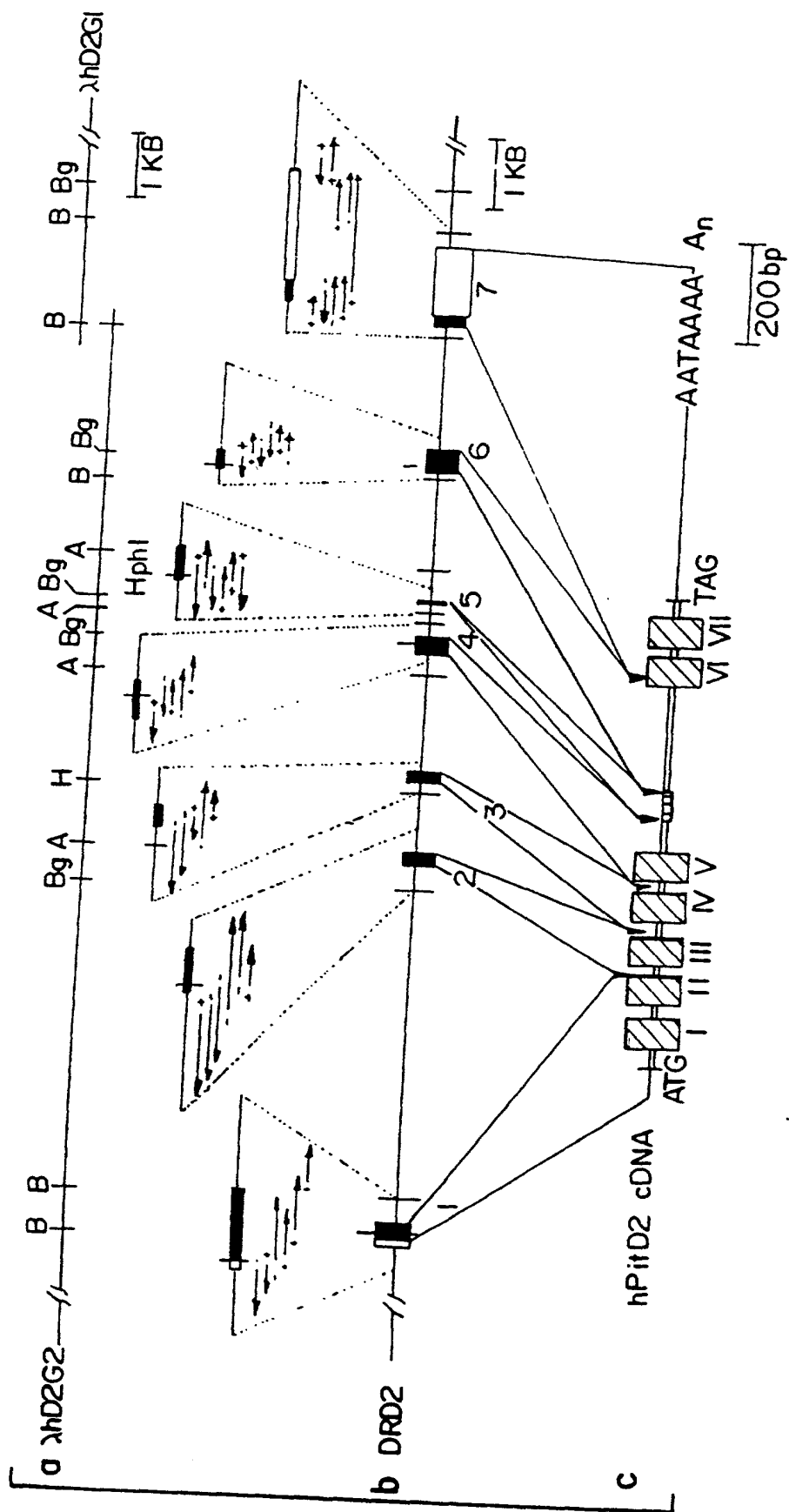
— 2.0

— 1.6

— 1.0

FIG. 20

FIG. 21



| DRUG | HUMAN D ₂ | RAT D ₂ | RAT STRIATUM |
|----------------------------------|----------------------|--------------------|--------------|
| PIPERONE | 0.125 | 0.35 | 0.56 |
| (+) BUTACLAMOL | 0.94 | 1.2 | 1.6 |
| HALOPERIDOL | 2.4 | 5.1 | 5.8 |
| SULPIRIDE | 206 | 160 | 205 |
| MIANSERIN (5-HT) | 2685 | 4300 | 4600 |
| SCH 23390 (D1) | 2145 | 2500 | 3300 |
| (+) BUTACLAMOL | >10,000 | >10,000 | >10,000 |
| Kd [³ H] DOMPERIDONE | 0.74 | 0.40 | 0.40 |

FIG. 22

FIG. 23

| | |
|------------------------|--------------------------------|
| 285 ¹ | 286 |
| exon1...GGAGgtagtg... | intron1...tccccagGTGG...exon2 |
| 395 | 396 |
| exon2...ACAGgtgagcc... | intron2...cttgcagGTAC...exon3 |
| 532 | 533 |
| exon3...GCAGgtacatt... | intron3...ccccccagACCA...exon4 |
| 723 | 724 |
| exon4...AAAGgtctcaa... | intron4...tccacagGGCA...exon5 |
| 810 | 811 |
| exon5...AGTGgtaagt... | intron5...gggtgcagGAGG...exon6 |
| 1138 | 1139 |
| exon6...CTCGgtgagtc... | intron6...ccccccagGGT...exon7 |

¹Numbering begins with A of the putative initiator methionine codon (see Fig. 18)